(19) Europäisches Patentamt
European Patent Office
Office européen des brevets

(11) EP 0 742 438 A2

(12) EUROPEAN PATENT APPLICATION

(43) Date of publication:
13.11.1996 Bulletin 1996/46

(51) Int. Cl.[6]: G01N 33/68, G01N 33/543, C07K 1/04, C07K 1/22

(21) Application number: 96106717.0

(22) Date of filing: 29.04.1996

(84) Designated Contracting States:
AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE

(30) Priority: 10.05.1995 US 438331

(71) Applicant: Bayer Corporation
Pittsburgh, PA 15219-2502 (US)

(72) Inventor: Buettner, Joseph A.
Raleigh, North Carolina 27614 (US)

(74) Representative: Burkert, Frank et al
Bayer AG,
Konzernzentrale RP,
Patente Konzern
51368 Leverkusen (DE)

(54) Screening of combinatorial peptide libraries for selection of peptide ligand useful in affinity purification of target proteins

(57) Ligands that interact with a target can be more easily identified if false positive interactions (either specific or non-specific) from the detecting system are differentiated from the target-specific interaction. An improved method of identifying peptides which bind with a target protein is presented. The steps are: binding a random library of peptides to a support material, allowing detection reagents to contact the peptides and the support material then identifying these interactions, then allowing the target protein to selectively bind to the peptides, allowing detection reagents to contact the bound target protein, and characterizing the peptide bound to the identified support material. Interaction of a ligand or the support material with the detection reagents will cause a distinct color change which distinguishes those ligands which selectively bind to target protein. The characterized peptide can then be used in affinity purification of the target protein. In one embodiment, automation of the assay is demonstrated by flowing all immunoreagents through the beads in a column format ensuring highly efficient washing. In the preferred embodiment, a resin for peptide synthesis which is hydrophilic, contains spacers and may exhibit less nonspecific background than other resins permits synthesis and direct evaluation of combinatorial peptide libraries for binding to target proteins is utilized. Examples for the use of this new resin and methodology for identifying peptide-ligands for purification of proteins are presented.

EP 0 742 438 A2

Description

Related Application U.S. Patent Application serial number 08/210,830 filed March 17, 1994 in the names of D.J. Hammond, et.al., entitled *Random Combinatorial Ligands for Affinity Chromatography of Target Molecule.*

BACKGROUND OF THE INVENTION

Field This invention is concerned generally with a method for the identification of ligands that bind to other molecules, and specifically, an identification method that distinguishes the target-specific ligand by differentiating it from ligands that specifically or non-sepcifically bind with the detection reagents used in the assay.

Background Peptide affinity columns offer substantial advantages over existing chromatography techniques for the purification of proteins (1). The power of this purification methodology, based upon known binding sequences, has been emphasized in the literature (2), but a major limitation has been the lack of known sequences which can act as ligands (1). The recent development of random peptide libraries (also called combinatorial, mimotope or epitope libraries) which contain a vast array of amino acid combinations for peptides of a defined length has allowed a rational approach to characterizing protein-peptide interactions (3-13).

Following the procedure first proposed by Scott and Smith (3), a hexamer (6 amino acid residues) library can be produced by splicing chemically synthesized oligonucleotides of random sequences (of 18 different nucleotide codons) into the coding region of a bacteriophage coat protein. Greater than 10^7 of the possible 10^{14} unique nucleotide codons can be represented with current phage-display technology (3-6). The phage are replicated in host ***Escherichia coli*** cells, harvested, and then incubated directly with the target protein immobilized on the surface of a culture dish (3). The phage that contain a peptide sequence that specifically interacts with the target protein are immobilized by the target protein while the phage that do not specifically bind to the target protein are lost in subsequent washing. The bound phage are harvested and processed so that the peptide that specifically binds the target protein can be identified.

However, methods for screening combinatorial libraries of ligands for affinity purification have major limitations: 1) phage displaying peptides that bind to the target protein must be isolated by biopanning; 2) the DNA of the binding phage must be sequenced; 3) before binding or purification with the peptides can be assessed, peptides must be synthesized and purified, and then chemical coupling of the ligands onto a chromatographic support must be done; and 4) the microenvironment of the peptide sequence presented on the surface of the chromatographic support may be very different from that presented by the phage which may radically affect the ability of the peptide to bind its target. These limitations have made the use of combinatorial libraries as a source of peptide ligands laborious and the identification of target protein-specific peptides uncertain.

In the mix, divide and couple synthesis first demonstrated by Furka (7), millions of unique peptide sequences are generated on polystyrene-based resinous beads. Subsequent improvements to the technique have allowed one to identify reactive sequences (10). However, identification of target-specific sequences by these binding assays has been compromised by high background staining from inefficient batch washing and the inherent inability to differentiate between sequences on beads that interact with the detection reagents from those that interact specifically with the target protein.

To overcome difficulties in distinguishing which unique peptide (bead) is interacting specifically with the target protein and which peptide (bead) is reacting with the detection reagents, I have synthesized peptides on a hydrophilic chromatographic resin and devised a two-step staining procedure that dyes beads reacting with the detecting reagents one color and those specific for target protein another. Typically this is performed with antibody-enzyme conjugates as the detecting reagents, although other reagents can be used. To create the most efficient washing conditions possible, we perform all assays in high pressure liquid chromatography (HPLC) columns, taking advantage of the flow-through characteristics of the resin. Each reagent is contacted with the beads as a separate HPLC injection with a wash program that removes non-specific binding by a salt gradient. Thus, automation of the assay is effected and run-to-run variations common with batch assays are eliminated.

In addition to the difficulties in identifying peptides that bind specifically to the target protein, the use of chromatographic media capable of providing the support for peptide syntheses and HPLC is limited. Most peptide synthesis supports are polystyrene-based resins that are inappropriate for use with biological assays. It is well known in the literature that polystyrene-based resins exibit both specific and non-specific interactions with various plasma proteins (11). To decrease non-specific binding to the detection reagents, hydrophilic peptide resins have been used in the synthesis and screening of peptides (12,13). Several polystyrene-based peptide synthesis resins have been rendered hydrophilic (8,9); these, however, are designed for chemical synthesis and not for direct biological assays (13), nor as large-scale chromatography supports.

Meldal, *et al.* have demonstrated the use of a commercially available acrylamide polymer resin modified for peptide library generation (12). Although appropriate for peptide synthesis and probing libraries, acrylamide resins do not have the chemical rigidity necessary for large scale high performance chromatography.

To overcome the problems associated with hydrophobic resins, I have developed a new modified resin which can be used for peptide synthesis, screening,

evaluation, and possibly final chromatographic use. The resin forming the basis of this invention is a polyhydroxylated methacrylate polymer commercially available from TosoHaas (14). The distinguishing characteristics of this resin are the inherent hydrophilic nature of the polymer, the large pore size (nominally 1000 angstroms), mechanical and chemical rigidity, and the graded ranges of bead diameters for direct applications in chromatography separations. This resin, after simple modification to generate a free amino group for peptide synthesis, shows good chemical resistance to classical peptide synthesis reagents.

This resin and the two-color staining assay have enabled us to identify peptide sequences that bind target proteins that, in contrast to the prior art, are selected to be specific only for the target protein and not the reagents. Beads binding to the detecting reagents are excluded by my method.

SUMMARY OF THE INVENTION

My invention is a procedure for determining which peptide in a combinatorial peptide library binds specifically with a target protein. The peptide library is bound to chromatographic supports and then incubated with the detecting reagents, resulting in a detectable change (e.g., a color change) of the support where the peptides or the support binds with the detecting reagents. The target protein is then added to the supports under conditions conducive to the target protein binding in a specific fashion to a peptide on the support. Detecting reagents are again added, this time resulting in a different change (e.g., a different color) which distinguishes the target protein bound specifically to the peptide from the prior, first change. In the preferred embodiment the detecting reagents are antibodies and their enzyme conjugates, and the procedure is performed using an HPLC apparatus, which serves as an efficient means for adding reagents and washing unreacted reagents from the system. The identified peptide can then be manufactured and bound to a chromatographic support for use in affinity purification of the target protein. The preferred support is hydrophilic and highly porous, having a preferred average pore size of about 800 to about 1200 angstroms, preferably about 1,000 angstroms. Although a preferred labeled detection system includes an enzyme-conjugated label (tag) which, depending on the substrate chosen, will permit generation of observable color changes, other lables or tags or combinations may be used (e.g. radio-labeled or fluorescent-labeled antibodies).

BRIEF DESCRIPTION OF THE FIGURES

Figure 1: Schematic of the two color immunostaining procedure.

A: Initial population of beads which have polypeptides (X_{1-6}) bound to them. The polypeptides on each individual bead have substantially the same sequence. The column is equilibrated by washing with buffers.

B: Add the first antibody (Ab^{TP}) and incubate, then rinse. Rinsing removes the loosely bound Ab^{TP}; what remains is non-specifically and specifically bound Ab^{TP} on the beads. N.B. Ab^{TP} is an antibody which specifically binds target protein.

C: Add the second antibody which is conjugated to enzyme (Ab*Enz). Incubate, and then rinse. What remains is Ab*Enz bound tightly and specifically to the bound Ab^{TP} and also bound non-specifically and specifically to the beads. N.B. Ab*Enz binds specifically to Ab^{TP}.

D: Add the blue dye substrate for the enzyme which dyes the enzyme bound beads a blue color. Incubate, then rinse out the excess blue dye.

E: Add the target protein (TP}). Incubate, and then rinse. The target protein specifically binds to a number of polypeptides among the population of beads.

F: Add Ab^{TP} and incubate, then rinse. The Ab^{TP} specifically binds TP}.

G: Add Ab*Enz. Incubate, then rinse. Ab*Enz specifically binds to Ab^{TP}.

H: Add red dye substrate for the enzyme which dyes the enzyme bound beads to a red color. N.B. Any remaining enzyme activity from the first color beads will result in those beads turning purple or brown.

I: Isolate red beads visually and subject single beads to peptide sequence analysis.

Figure 2: Chromatogram of the immunoassay technique for Ribonuclease S (RNase S) protein injected on the YNFEVL-TSK resin diluted (1:20 w/w) with TSK-Blank. The upper line (A) is the absorbance at 280 nm; the middle line (B) is the flow

rate, and the lower line (C) indicates the gradient conditions.

Figure 3: Validation of the HPLC Affinity assay by RNase S protein and peptide-resin (YNFEVL-TSK). The top figure shows the 280 nm absorbance profile for Human Serum Albumin (HSA) (A) and RNase S protein in HSA (B). The bottom figure is the pressure tracing from chromatogram B.

Figure 4A: Chromatograms of Factor IX binding to YANKGY-TSK. The bottom trace (A) is a buffer blank. The middle trace (B) is the carrier protein (1.0 mL of 0.5% HSA). The top trace shows that 55 µg of Factor IX injected onto the column is released during the acid wash.

Figure 4B: This figure shows the Factor IX peak from the chromatogram in Fig 4A at increased scale.

Figure 5: Chromatograms of various amounts of Factor IX injected onto YANKGY-TSK. The bottom trace (A) is 55 µg of Factor IX without HSA. Trace B is 110 µg of Factor IX and C is 220 µg Factor IX, both without HSA. The D trace is 220 µg of Factor IX heated at 95°C for 5 min prior to injection. The top trace (E) is 220 µg Factor IX in HSA.

Figure 6: SDS-PAGE (Fig. 6A) and Western blot (Fig. 6B) of mixtures of Factor IX and HSA. Lanes 1 and 9 are molecular weight standards. Lane 2 is Factor IX (Enzyme Research Labs; South Bend, IN). Lane 3 is an HSA standard (Miles Inc.) Lane 4 is the starting material that was injected onto the YANKGY-TSK affinity column (1.0 ml, 220 µg of Factor IX in HSA). Lane 5 is the first flow-through peak. Lane 6 is the second flow-through peak. Lane 7 is the NaCl wash. Lane 8 is the acid eluted peak. Approximately 10 µg of total protein was loaded into each lane.

Figure 7: Chromatogram (Fig. 7A), SDS-PAGE (Fig. 7B) and Western blot (Fig. 7C) of 1.0ml citrated human plasma on the Acetyl-YANKGY-TSK resin. Approximately 10ug were loaded in each lane and the electroblotted gel was loaded with the same amount of sample as the Coomassie stained gel. Lanes 1, 5, 7, 9, and 11 were blank. Lane 2: 1.0ug of Factor IX; Lane 12: 0.0625ug of Factor IX. Lanes 3 and 13: molecular weight standards. Lanes 4 and 15: human plasma. Lane 6: flow through (t= 0 to 12min); Lane 8: flow through (t = 12 to 15min). Lane 10: the acid eluate. Lane 14: a partially-purified Factor IX intermediate. The Western blot on the lower right shows no Factor IX in the starting material or flow throughs. A strong immuno-detected band corresponding to the Factor IX zymogen is in the acid eluate.

SPECIFIC AND PREFERRED EMBODIMENTS

Materials and Methods

Resin Chemistry For peptide synthesis, a polyhydroxylated methacrylate-type chromatography resin, preferably Toyopearl 650M Chelate (65 µm particle size, 1000 Å pore size; TosoHaas, Montgomeryville, PA) was rinsed in a 25g reaction vessel with water, methanol and dimethylformamide (DMF). A five-fold molar excess of ethylenediamine over resin carboxylate was coupled onto the carboxylate moiety with a slight molar excess of benzotriazole-1-yl-oxy-tris-pyrrolidinophosphonium hexafluorophosphate (PyBOP, Novabiochem, La Jolla, CA) and N-methylpyrrolidinone (NMM, three-fold molar excess over PyBOP; Aldrich Chemical Co.; Milwaukee, WI) in DMF for 60 minutes. The aminated resin was washed with DMF, then methanol, then dried *in vacuo*.

To generate a non-cleavable resin, two standard solid phase peptide synthesis couplings followed to introduce two molecules of β-alanine (Novabiochem) spacer residues (referred to as TSK-Blank). To generate a cleavable resin for soluble peptides a two-fold molar excess (over amine on the beads) of p-[(R,S)-α-[1-(9H-Fluoren-9-yl)-methoxyformamido]-2,4-dimethoxybenzyl]-phenoxyacetic acid (Novabiochem) was activated with a slight molar excess of PyBOP and NMM, then added to the aminated TSK-Blank resin. Coupling was allowed to proceed for 4 hours, with subsequent DMF and methanol washes. Other linkage chemistries, which are widely known by those practiced in the art, and are compatible with the functional moieties available on different polyhydroxylated methacrylate resins, can be used. A commercially available Rink amide resin was used for comparison.

Combinatorial Library Peptide Chemistry Combinatorial peptide libraries were generated in a manner similar to Furka (7). A large-scale synthesis block in the multiple peptide synthesizer was used to perform each coupling in a semi-automated manner. One-half gram of dried, aminated TSK-Blank resin was added to each of 18 reaction vessels and 18 of the 20 naturally occurring L-amino acids (in this embodiment I omitted cysteine and methionine; however, this is not a requirement for the utilization of this invention) were coupled by standard FMOC chemistry (see below). The resin from each

vessel was pooled and washed in DMF with argon agitation. The resin was equally redistributed into the 18 reaction vessels and the next amino acid was coupled as the first. This was repeated until the hexamer library was complete (two working days). The resin was pooled, washed with methanol, dried *in vacuo*, then deblocked with Reagent R (18) (90% trifluoroacetic acid (TFA), 5% thioanisole, 3% ethanedithiol, 2% anisole; all from Aldrich) for 3 hours with argon agitation. The resin was washed with 20 column volumes of methanol, then dried *in vacuo*.

Batch Peptide Synthesis Peptide sequences were synthesized by the solid phase method (15) on a Gilson AMS422 Multiple Peptide Synthesizer (16) with FMOC as α-amino protection (16, 17). Depending on whether or not the peptides would be cleaved from the beads for analysis, either the aminated-cleavable TSK-Blank resin, or the non-cleavable TSK Blank resin, or the Rink resin (for comparison) were used as the synthesis support. Large scale single couplings of amino acids (5-fold molar excess; 1 mL of 0.5M in DMF) were activated *in situ* with PyBOP (0.5 mL of 0.3M in DMF) and NMM (0.25 mL of 1.19M in DMF) with our modified TosoHaas resin (0.3g, 200 μmoles) or Rink amide resin (0.5g, 200 μmoles). Coupling was allowed to proceed with argon bubbling agitation for 45 minutes. All peptides were cleaved and/or blocked with Reagent R for 3.5 hours.

For affinity chromatography analysis, the TSK non-cleavable resin-peptides were deprotected (as generally practiced in the art) in the synthesis vessel, extensively washed with methanol and dried *in vacuo*. For peptide analysis, the TSK cleavable and the Rink peptide-resins were cleaved and deprotected in 20 mL scintillation vials. These peptide mixtures were filtered away from the resin directly into 40 mL cold anhydrous diethyl ether (Aldrich) through a medium porosity sintered glass funnel. The filter cakes of peptides were dissolved in 50% acetonitrile/water and lyophilized in a tared scintillation vial. These precipitated, unpurified peptides were dissolved at 25-50 mg/mL in 50% acetonitrile/water and 1 mL was purified by preparative HPLC (Gilson, Inc.) with a 22 mm X 250 mm (C18 15u 300Å) reverse phase column (Vydac; Hesperia, CA). To ascertain purity, crude peptides were dissolved at 10 mg/mL in 50% acetonitrile/water and purified peptides were dissolved at 10 mg/mL in 20% acetonitrile/water. 10 μL aliquots were analyzed by microbore HPLC (Ultrafast Microprotein Analyzer, Michrom BioResources, Inc.; Sacramento, CA) with a 2.1 mm x 150 mm C18 5u 300Å reverse phase column and a 2 to 60% acetonitrile gradient in water over 12 minutes.

Analyses Amino acid analysis was performed as described by Spackman (20) with a 6300 Amino Acid Analyzer (Beckman Instruments, Inc.; Fullerton, CA) using ninhydrin detection. Peptide mass determinations were performed by positive ion fast atom bombardment (FAB) ionization on a JEOL HX-110 double focusing mass spectrometer. The peptides were spotted in 50% acetonitrile/water onto a thioglycerol matrix. The mass range scanned depended upon the expected mass of the peptide. Peptide sequencing was performed by Edman chemistry using an ABI 477A Protein/Peptide Sequencer (Applied Biosystems; Foster City, CA) interfaced with a 120A HPLC (C18 PTH, reverse-phase chromatography) Analyzer to determine phenylthiohydantoin (PTH) amino acids. Sandwich ELISAs were performed as described by Bessos (21). Protein samples were quantitated by the Biuret assay (22), then analyzed by SDS-PAGE (23) and Western blot techniques (24).

HPLC Library Immuno-Assays To differentiate between detecting reagent-binding and target-binding peptide-resin beads, we developed a two color peptide library staining chromatography technique. Figure 1 is a schematic of the preferred embodiment of the technique. All assays were performed on an Ultrafast Microprotein Analyzer in a 2.1 mm I.D. X 150 mm long stainless steel column (volume = 520 μL) at 37°C. Dry library resin was packed into the column by vacuum, then the column was attached to the detector flow cell and washed with 20 column volumes of 20% methanol/water, 5 column volumes of 100% Buffer A (10 mM HEPES, 100 mM NaCl, 2.5 mM Ca Cl_2, 20 mg/mL D-mannitol; all from Sigma Chemical Co.; St. Louis, MO), then 5 column volumes of 50% Buffer B (Buffer A with 1.0 M NaCl) to clean the resin. The complete assay comprised of seven chromatography injection programs sequentially linked and executed as a batch (EXChrom Chromatography Data System, Scientific Software, Inc.; San Ramon, CA). Each injection program was 90 min long. At the start of each injection program, a 1.0 mL sample loop of reagent was injected at 200 μL/min for 3.5 min, then allowed to perfuse the column at 5 μL/min for 50 min before the flow increased to 400 μL/min for the duration of the run. At 60-75 min, a salt gradient from 0.1 M to 1.0 M NaCl eluted non-specific binding proteins. This high salt buffer was used to wash the column for 15 min, then the column was reequilibrated to the original conditions.

For each assay batch there were 7 injections: 1) Buffer A blank; 2) 0.5% Human serum albumin (HSA; Miles, Inc., Clayton, NC) without target protein (fig. 1A); 3) 1:1000 diluted first antibody (fig. 1B); 4) 1:1000 diluted second antibody-alkaline phosphatase conjugate (fig. 1C). Each immunoreagent was diluted in 0.5% HSA in Buffer A. After the fourth injection program, the batch job was stopped for the first staining process. In this particular example, the buffer flow was stopped, the column disconnected and the resin extracted with 100% Buffer A at 300 μL/min. 15 fractions (2 drops per fraction) were collected into a 24 well microtiter plate (Corning/Costar).

BCIP/NBT was added and the staining performed in the well. Visual observation of the staining process allowed for optimal staining times. Alternatively, the staining can be accomplished in the column, making the entire procedure fully automated (fig. 1D). The stained resin fractions were loaded into 3 mL reaction tubes,

washed extensively with water, dried *in vacuo*, then dry packed back into the column in the same order the resin was fractioned. TSK-Blank resin was used to fill the column outlet to replace any lost resin. After re-equilibrating the column, target protein (2.4 pmole sample amount in Buffer A with 0.5% HSA) was injected (injection program number 5) (fig. 1E). The following two injection programs, 6 and 7, were the same as program numbers 3 and 4 (fig. 1F & 1G). After these programs were complete, the resin beads were fractionated as before, then stained with Fast Red in the microtiter plate wells and inspected visually.

Affinity Purification of Target Protein Affinity purification of target protein was used to assess the ability to purify proteins with the peptide sequences identified as being specific. Individual library-derived sequences that were found to bind to target proteins were synthesized in a batch format on TSK-Blank resin as described above. The deprotected peptide-resin was dry packed into a blank column as described above and washed with 20 column volumes of 20% methanol/water, then 10 column volumes of Buffer A, and assayed by sequential 1.0 mL injections of 1) Buffer A blank, 2) 0.5% HSA, and 3) target protein in 0.5% HSA. Non-specifically bound proteins were washed off the column in a step gradient of 1.0 M NaCl for two column volumes, and the target protein was eluted from the column in a weak acid solution.

Validation of the HPLC Library Immunoassay

Ribonuclease S protein In this embodiment, the HPLC assay was validated by the use of a control binding peptide for a specific target protein. The previously identified RNase S protein-binding peptide (25), YNFEVL, was synthesized on TSK-Blank resin as taught in the previous section, then diluted with TSK-Blank until the final ratio of peptide-resin to TSK-Blank was 1:20 of the total weight. Figure 2 shows the microbore HPLC injection program of the UV trace, flow profile and gradient conditions of the immunoassay technique using RNase S protein as the target protein (HSA is the protein carrier). Red beads (indicating target protein interacting with the YNFEVL-TSK resin beads) were found at the frequency of 5% throughout the column demonstrating the column is not depleted of target or immunoreagents during the peptide library immunostaining chromatography runs. Also present were clear white beads from the TSK-Blank which showed no reactivity with the detection system or the RNase S protein. Dark blue beads which indicate non-specific or immunoreagent-specific interactions were present only at a very low frequency (less than 0.01%). Some beads became chipped or scored during the process of syntheses, cleavage, or chromatography analysis, but in general, the integrity of the beads as a chromatography support did not appear to be compromised as the beads did not collapse upon high pressures (greater than 4,000 psi).

Validation of the HPLC Affinity Chromatography Method

Ribonuclease S Protein Affinity Chromatography In this embodiment the HPLC affinity methodology is validated by the previously described Rnase S protein/YNFEVL peptide system. Peptide synthesis was performed as taught in the previous section. Figure 3 shows the HPLC affinity chromatography analysis of RNase S protein. 42 nmoles of RNase S protein was injected in a 1.0 mL volume onto the column at 200 µL/min for 3 min. The flow was decreased to 5 µL/min for 5 min to perfuse the column, then increased to 400 µL/min to wash off the unbound protein. At 13 min, an injection of 1.0 mL Buffer A with 1.0 M NaCl eluted non-specific binding proteins, then the column was returned to 0.1 M NaCl until 19 min when a steep gradient to 2 % acetic acid in water and a flow of 800 µL/min began. After 5 min, the column returned to Buffer A to equilibrate the resin. The peak at 22 min represents the target protein eluted in the acid wash.

EXAMPLE

Hexamer Library-Factor IX Target A hexamer peptide library was assayed with the this peptide library immunostaining chromatography assay for its ability to bind the serine protease Factor IX zymogen. The library was assayed as described and several red bead sequences were found. Individual stained beads were hand picked with a pipette under a dissecting microscope. Of the 6 beads isolated from two independent analyses, two beads gave a clear sequence (YANKGY and YNYFNQ). The amount of peptide per bead was found to be approximately 10 pmoles (0.1 meq/g), which is sufficient for sequencing.

Factor IX/Albumin Affinity Purification The library-derived peptide identified above binds and purifies a mixture of a commercially available, highly purified Factor IX zymogen in a solution of human serum albumin. The YANKGY sequence was batch synthesized as described and quantitative amino acid analysis showed the proper sequence. This peptide-resin was tested for its ability to bind Factor IX. Figure 4 shows the chromatograms, demonstrating that the YANKGY peptide ligand synthesized on the TSK-blank does bind Factor IX. HSA bound to the column to a small extent. However, this was eluted by the salt wash as evidenced by the absence of a peak during the acid elution. In contrast, when Factor IX was added to the HSA, there was a distinct peak eluted by the acid. This demonstrates that the target protein (Factor IX) bound the peptide with sufficient avidity to indicate specificity.

Figure 5 shows the chromatograms for increasing amounts of Factor IX added to the column. A direct correlation was seen between the acid peak area and the amount of Factor IX injected. Heating Factor IX for 5 min decreased binding to the column, as demonstrated by the decrease of the acid peak area. The top chromato-

gram in Figure 5 shows the UV trace of 220 µg of Factor IX in HSA. The acid peak area from this run (Figure 6, lane 5) was not significantly different in peak area to that of Factor IX without HSA (Figure 6, lane 3), consistent with the Factor IX being separated from HSA. Aliquots of fractions taken from this run were assayed for Factor IX detection by ELISA (data not shown). No Factor IX was detected in the flow through peak (from Figure 5, top trace); 17% of the amount of Factor IX injected was detected in the NaCl peak; and 25% in the acid peak. Factor IX may be partially denatured during the acid elution which could account for the lack of full recovery based on ELISA results. Indeed, controls of adding acid to Factor IX prior to analysis in the ELISA do show a 40 to 50% decrease in the ELISA signal. The remainder of the fractions were precipitated in cold (-20°C) acetone and analyzed by reducing SDS-PAGE, normalizing sample to total protein. Figure 6 shows that there is a clear purification of Factor IX from HSA. Binding of Factor IX to the YANKGY-TSK column was confirmed by Western blot analysis: a very light Factor IX band was seen in the starting material and no detectable Factor IX was seen in either flow-through fraction but dark bands corresponding to Factor IX were seen in both the NaCl wash and the acid peak.

Plasma-Derived Factor IX Affinity Chromatography

The relevance of this library-derived peptide ligand is to purify human Factor IX zymogen from unpurified human plasma. A 1.0ml injection of human citrated plasma was contacted with an acetyl-YANKGY-TSK column in the manner taught in the above example. Flow through and acid peaks were collected on ice and immediately assayed for total protein, SDS-PAGE and Western blot analyses. Figure 7 shows the purification chromatogram, SDS-PAGE and Western blot of the fractions collected. Samples were normalized to total protein as described before. There are numerous protein bands in the starting material, the predominant being albumin. The Factor IX band is not visible in any fraction in the Commassie stained gel. The blot shows no Factor IX in the starting material (it is below the sensitivity of the detection system), no Factor IX in the flow through, yet a very large band in the acid peak. With one pass over the YANKGY-TSK affinity column, analyzing total protein and by Western blot, the approximate purification was 200 fold from plasma. This demonstrates conclusively that this library-derived sequence binds and purifies the Factor IX zymogen from human plasma.

Other Detection System for this HPLC Assay

Noncolorimetric detecting systems. It can be further appreciated by those skilled in the art that the invention can easily be extended to use different reagents which are functionally equivalent to those used in previous examples. Antibody-conjugates are the preferred embodiment; however, target-enzyme direct conjugates can also be used with this technique. It is well known in the art that the peptide sequence HPQ will bind streptavidin. If this sequence were contained in a peptide library it could be identified by this two color library staining chromatography technique. In this example the third injection should contain some kind of labeling molecule capable of imparting color to the bead (like a phosphatase molecule). The column would be extracted, and the first color reagent (NBT/BCIP) would be applied to the beads. The column would be repacked as described before, and the target injection would be streptavidin conjugated to phosphatase. With subsequent addition of the differential staining reagent (Fast Red) the beads stained the second color would be specific for the streptavidin target.

Moreover, the staining reagent does not have to be an enzyme. Any tag that imparts a signal could be utilized to differentiate the ligands that react with the detecting system from those that react with the target. For example, fluorescent molecules imparting different colors could be used with identification by fluorescence-activated cell sorting; radioactive isotope tags (125I/131I or 35S-Met/75Te-Met) could be identified in autoradiograms or by scintillation counting; or non-radioactive isotope tags (e.g. 14N/15N) could be identified by NMR; or mixed mode color identification where the beads interacting with the detecting reagents are colored as described above and the target-specific beads are identified by luminescence with disodium 3-(4-methoxyspiro(1,2-dioxetane-3,2'-(5' chloro) tricyclo (3.3.1.13,7) decan)-4-yl) phenyl phosphate (CSPD, Tropix, Bedford, MA) or any other luminescing reagent.

CONCLUSION

In conclusion, a method has been developed that can quickly identify combinatorial library-derived sequences that are target specific. This two color, peptide library immunostaining chromatographic analysis has been used to identify sequences that bind to the coagulation cascade Factor IX zymogen. The technique has been validated using a peptide sequence which is known to bind Ribonuclease S protein. This technique has further been extended to use the identified peptide ligand to construct an affinity chromatography medium for the purification of the target protein.

This method lends itself to additional useful experimental schemes. By using a strategy of combinatorial resin modification with this two color, peptide library immunostaining chromatographic analysis, chromatographic substrate modifications useful for separations of molecules of similar structure (e.g., isoforms of proteins, or the same proteins from different sources, such as sheep alpha 1 proteinase inhibitor from transgenic human alpha-1 proteinase inhibitor expressed in the sheep's milk) can be identified. In these examples an isoform of the target molecule may be included in the first half of the assay to generate the first color. The different isoform may be included in the second half of the assay to generate the second color. Thus, specificity for

the second isoform would be identified by the beads dyed by only the second color.

Binding interactions are important pharmacologically, thus this strategy can be useful for lead identification in drug discovery. For example, a peptide library may be probed with soluble cellular receptors like the soluble form of the epidermal growth factor receptor or the soluble form of the erythropoietin receptor to identify peptide ligands of potential pharmacological significance. A large pore size of the resin is necessary in order to provide full access to the peptide for these large proteins. The method also may be used to identify binding interactions between other kinds of (i.e. non-peptidic) molecules. We have also found this method useful for quick evaluation and optimization of ligands derived from screening phage libraries.

The above examples are intended to illustrate the invention and it is thought variations will occur to those skilled in the art. Accordingly, it is intended that the scope of the invention should be limited only by the claims below.

REFERENCES

1. Baumbach, G.A., Hammond, D.J., Biopharm. **5** 24 (1992)

2. Huang, P.Y., Carbonell, R.G., Biotechnol. and Engin., *in press*

3. Scott, J.K., Smith, G.P., Science **249** 386 (1990)

4. Devlin, J.J., *et al.*, Science **249** 404 (1990)

5. Cwirla, S.E., *et al.*, PNAS **87** 6378 (1990)

6. Folgori, A., *et al.*, EMBO **13** 2236 (1994)

7. Furka, A. *et al.*, Int. J. Pept. Protein Res. **37** 487-493 (1991)

8. Zalipsky, S., *et al.*, in *Peptides: Structure and Function, Proceedings of the Ninth American Peptide Symposium* (Deber, C.M., Hruby, V.J., & Kopple, K.D. eds.), p.257. Pierce Chemical Co., Rockford, IL (1985)

9. Bayer, E., Rapp, W., *Chemistry of Peptides and Proteins* **3** (Ovchinnokov, Y.A., ivanov, V.T., eds.)

10. Lam, K.S., *et al.*, Nature **354** 82-84 (1991)

11. Boisson-Vidal, C., *et al.*, Biomedical Materials Res., **25** 67-84 (1991)

12. Meldal, M., *et al.*, Proc. Natl. Acad. Sci. USA **91** 3314-3318 (1994)

13. Vagner, J., *et al.*, *Innovative Perspectives in Solid Phase Synthesis* (Epton, R., ed.), in press

14. Kato, Y., *et al.*, J. Chromatography **354** 511-517 (1986)

15. Merrifield, R.B., Fed. Proc. **21** 412 (1962).

16. Gausepohl, H., *et al.*, Peptide Research **5** 315-320 (1992)

17. Atherton, E., *et al.*, J. Chem. Soc. Chem. Commun. 539-540 (1978)

18. Fields, G.B., *et al.*, Int. J. Pept. Prot. Res. **35** 161 (1990)

19. Albericio, F., *et al.*, J. Org. Chem. **55** 3730-3743 (1990)

20. Spackman, D.H., *et al.*, Anal. Chem. **30** 1190 (1958)

21. Bessos, H., *et al.*, Thrombos. Res. **40** 863 (1985)

22. Davis, E.M., Am. Biotech. Lab., July 28 (1988)

23. Laemmli, U.K., Nature **277** 680 (1970)

24. Bowen, P., *et al,*, Nuc. Acids Res. **8** 1 (1980)

25. Smith, G.P., *et al.*, Gene **128** 37-42 (1993)

Claims

1. In a method of selecting a ligand which will bind to a target substance, the ligand being in a population of individual random ligands bound to individual support materials, and the selection being with a labeled signal-providing detection system, the improvement which comprises incubating the population of random ligands with components from the detection system prior to any contact of the population of ligands with the target substance such that, after contact with the target substance, the reagents of the labeled detection system can then be contacted again with the ligand population and used to generate a different a different signal to allow detection of the ligand which binds to the target substance against the background of the random ligands which do not bind to the target substance.

2. The method of claim 1 wherein the labeled detection system includes an enzyme-conjugated tag.

3. The method of claim 2 wherein the tag is an antibody.

4. The method of claim 1 wherein the labeled detection system includes a radioisotope-labeled tag.

5. The method of claim 4 wherein the tag is an antibody.

6. The method of claim 1 wherein the labeled detection system includes a fluorescent-labeled tag.

7. The method of claim 6 wherein the tag is an antibody.

8. The method of claim 1 wherein the labeled detection system includes any combination selected from an enzyme-conjugated antibody, a radio-labeled antibody and a fluorescent-labeled antibody.

9. The method of claim 1 wherein the ligand is a peptide and the target substance is a protein selected from plasma proteins and proteins expressed from a genetically engineered cell or hybridoma.

10. The method of claim 9 wherein the peptide comprises about 3 to 10 amino acid residues.

11. The method of claim 9 wherein the protein is Factor IX.

12. The method of claim 1 wherein the support material is a resin.

13. The method of claim 12 wherein the support material is hydrophilic.

14. The method of claim 12 wherein the support material is porous.

15. The method of claim 14 wherein the average pore size ranges from about 800 to about 1200 angstroms.

16. The method of claim 1 where the steps occur in an HPLC column.

17. The method of claim 14 wherein the pressure of the HPLC column is about 0 psi to 4000 psi.

18. A method of identifying peptide ligands which bind with a specific target protein comprising:

(a) immobilizing randomized peptides on individual chromatographic supports to create a population of supports, each support bead having bound to its surface peptides substantially identical to each other;

(b) contacting the supports of step (a) with a first antibody capable of specifically binding to the target protein, under conditions that allow both specific and nonspecific binding to the target protein, said first antibody also capable of binding specifically and non-specifically to both the supports and peptides on the support;

(c) contacting the supports of step (b) with a second antibody capable of specifically binding to the first antibody and having conjugated thereto an enzyme capable of reacting with at least two different substrates to produce two different color changes, under conditions sufficient to bind the second antibody to the first antibody, said second antibody also capable of binding specifically and non-specifically to both the supports and peptides on the support;

(d) adding a first substrate to the supports of step (c) under conditions sufficient to cause a first color change on individual supports having bound thereto the second antibody;

(e) adding the target protein to the supports of step (d) under conditions sufficient to allow specific binding of the target protein to at least one of the peptides bound to the supports;

(f) contacting the supports of step (e) with the first antibody of step (b) under conditions sufficient to bind that antibody specifically to the target protein;

(g) adding the second antibody of step (c) having the enzyme conjugated thereto to the supports of step (f) under conditions sufficient to bind the second antibody specifically to the first antibody bound to the target protein bound to the peptides bound to the supports;

(h) adding a second substrate to the supports of step (g) under conditions sufficient to cause a second and different color change which distinguishes those supports having bound thereto the peptides which bind with the target protein;

(i) separating the supports having the peptide that binds to the target protein on the basis of the color change caused by the preceding step; and

(j) sequencing the peptide on the support separated in step (j).

19. The method of claim 18 wherein there are wash steps between steps (a) and (b), (b) and (c), (c) and (d), (e) and (f), (f) and (g), and (g) and (h).

20. The method of identifying peptides according to claim 19, wherein the support material comprises

porous hydrophilic resin beads having an average pore size ranging from about 800 to about 1200 angstroms.

21. The method of identifying peptides of claim 18 wherein the peptides have a length ranging from about 3 to 10 amino acid residues.

22. The method of claim 18 wherein the supports are contained within a column.

23. The method of claim 20 wherein the column is attached to an automated chromatography apparatus.

24. In a method of identifying a ligand molecule that binds to a target molecule, wherein the method comprises:

using the target molecule to probe a random library of ligand molecules immobilized upon a substrate, and then

using detection reagents to change an observable characteristic, said change of observable characteristic indicating binding between the target molecule and the ligand molecule upon said substrate,

the improvement of which comprises the further step of:

prior to probing the random library with the target molecule, using the detection reagents to probe the random library, said probing with the detection reagents causing a different change of observable characteristic, said different change of observable characteristic indicating reaction of the detection reagents with the library of ligand molecules immobilized upon said substrate and serving to distinguish binding between the target molecule and the ligand molecule from reaction of the detection reagents with the library of ligand molecules immobilized upon said substrate.

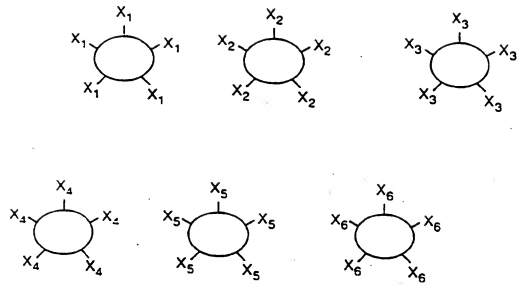


FIG._1A

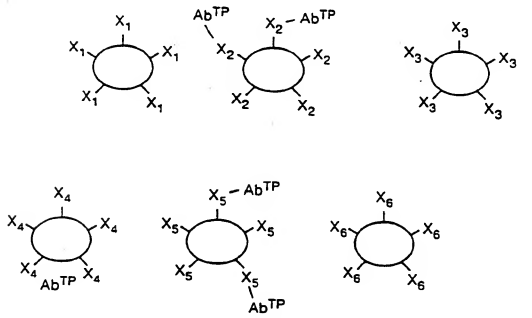


FIG._1B

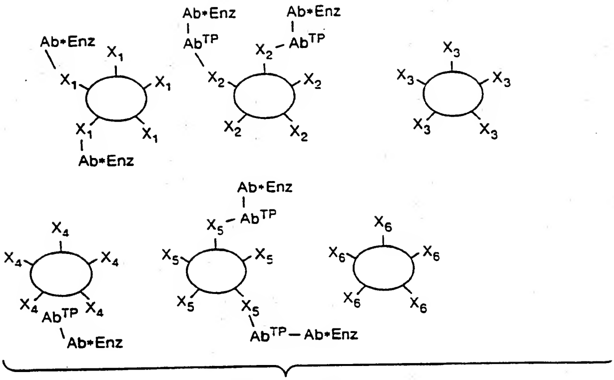


FIG._1C

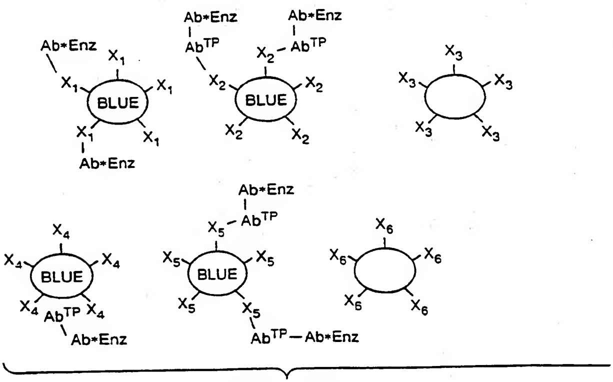


FIG._1D

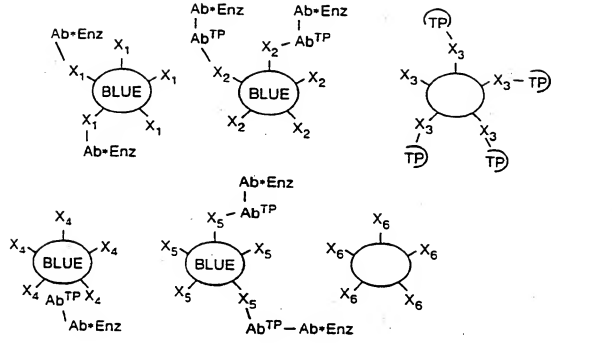


FIG._1E

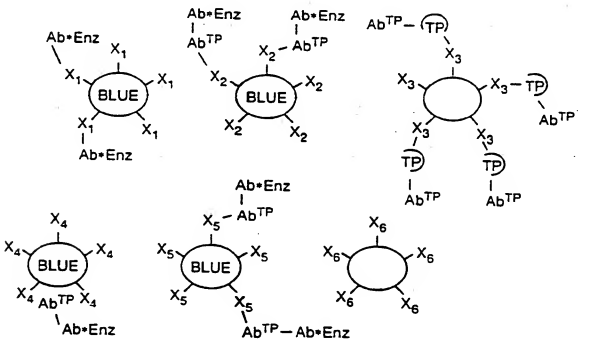


FIG._1F

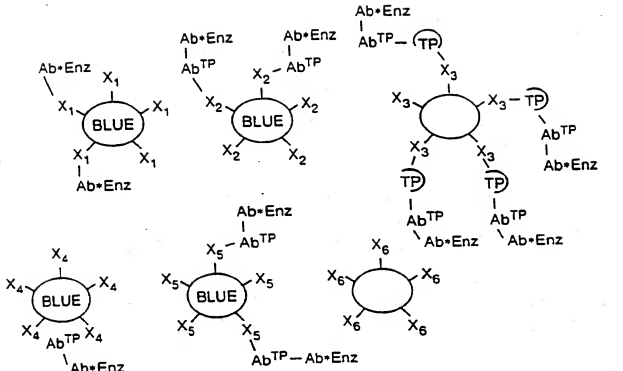


FIG._1G

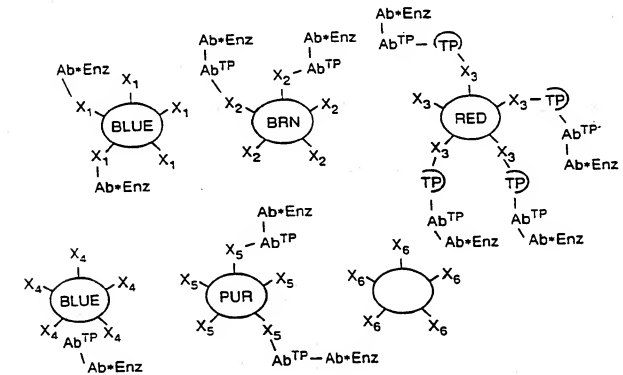
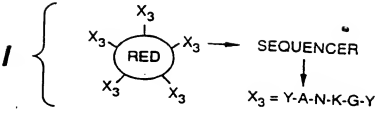


FIG._1H

FIG._1I



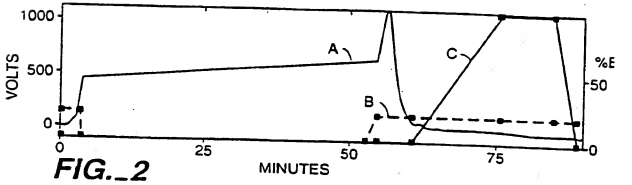


FIG._2

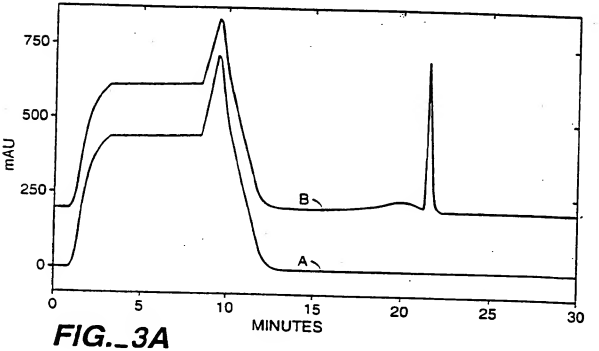


FIG._3A

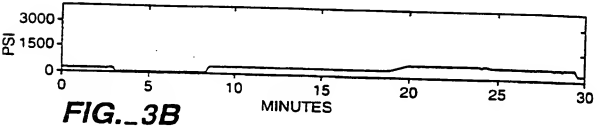


FIG._3B

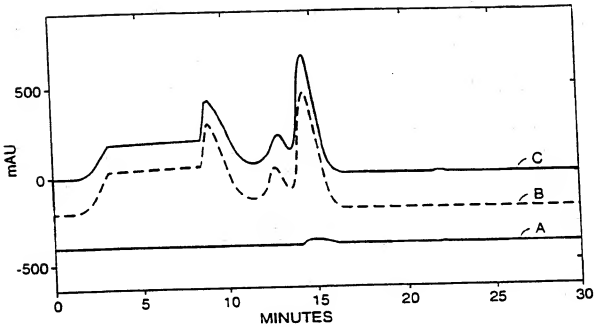


FIG._4A

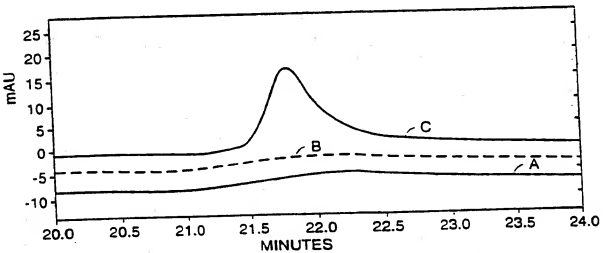


FIG._4B

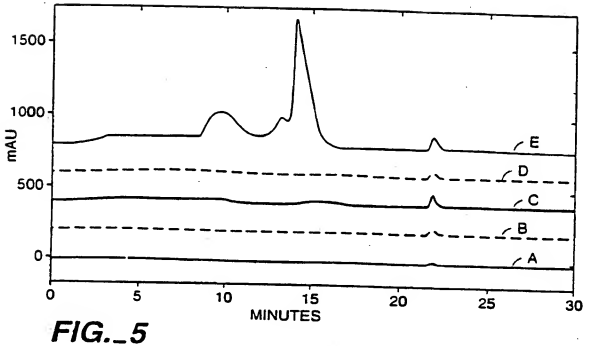


FIG._5

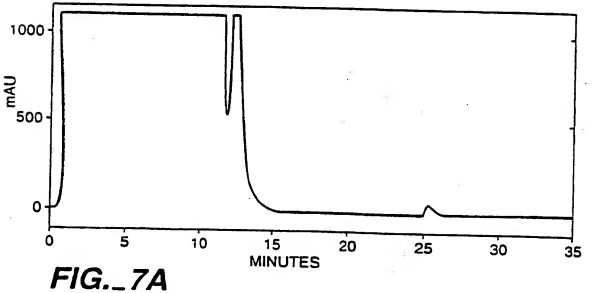


FIG._7A

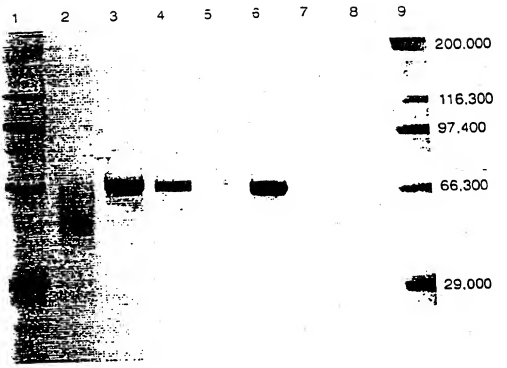


FIG._6A

FIG._6B

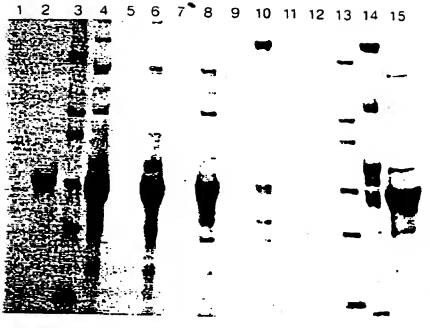


FIG._7A

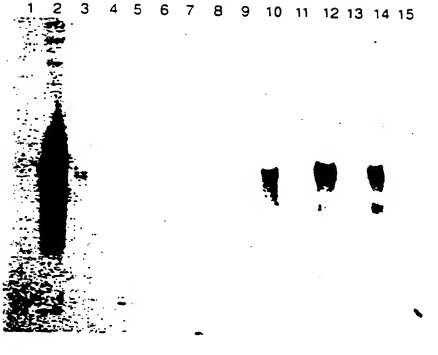


FIG._7B

(19) Europäisches Patentamt
European Patent Office
Office européen des brevets

(11) EP 0 742 438 A3

(12) **EUROPEAN PATENT APPLICATION**

(88) Date of publication A3:
08.04.1998 Bulletin 1998/15

(43) Date of publication A2:
13.11.1996 Bulletin 1996/46

(21) Application number: **96106717.0**

(22) Date of filing: **29.04.1996**

(51) Int. Cl.[6]: **G01N 33/68**, G01N 33/543, C07K 1/04, C07K 1/22

(84) Designated Contracting States:
AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE

(30) Priority: **10.05.1995 US 438331**

(71) Applicant: **Bayer Corporation**
Pittsburgh, PA 15205 (US)

(72) Inventor: **Buettner, Joseph A.**
Raleigh, North Carolina 27614 (US)

(74) Representative:
Burkert, Frank et al
Bayer AG,
Konzernbereich RP
Patente und Lizenzen
51368 Leverkusen (DE)

(54) Screening of combinatorial peptide libraries for selection of peptide ligand useful in affinity purification of target proteins

(57) Ligands that interact with a target can be more easily identified if false positive interactions (either specific or non-specific) from the detecting system are differentiated from the target-specific interaction. An improved method of identifying peptides which bind with a target protein is presented. The steps are: binding a random library of peptides to a support material, allowing detection reagents to contact the peptides and the support material then identifying these interactions, then allowing the target protein to selectively bind to the peptides, allowing detection reagents to contact the bound target protein, and characterizing the peptide bound to the identified support material. Interaction of a ligand or the support material with the detection reagents will cause a distinct color change which distinguishes those ligands which selectively bind to target protein. The characterized peptide can then be used in affinity purification of the target protein. In one embodiment, automation of the assay is demonstrated by flowing all immunoreagents through the beads in a column format ensuring highly efficient washing. In the preferred embodiment, a resin for peptide synthesis which is hydrophilic, contains spacers and may exhibit less nonspecific background than other resins permits synthesis and direct evaluation of combinatorial peptide libraries for binding to target proteins is utilized. Examples for the use of this new resin and methodology for identifying peptide-ligands for purification of proteins are presented.

EP 0 742 438 A3

European Patent Office

EUROPEAN SEARCH REPORT

Application Number
EP 96 10 6717

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
X	LAM K S ET AL: "Application of a dual color detection scheme in the screening of a random combinatorial peptide library" JOURNAL OF IMMUNOLOGICAL METHODS, vol. 180, no. 2, 27 March 1995, AMSTERDAM NL, pages 219-223, XP004021044 * the whole document * ---	1-10,18, 24	G01N33/68 G01N33/543 C07K1/04 C07K1/22
A	EP 0 473 065 A (ABBOTT LABORATORIES) * page 2, line 50 - page 5, line 35 * ---	1-8	
D,A	KATO Y ET AL.: "High-performance metal chelate affinity chromatography of proteins" JOURNAL OF CHROMATOGRAPHY, vol. 354, 1986, AMSTERDAM NL, pages 511-517, XP002053925 * the whole document * ---	1,12-15	
P,X	BUETTNER J A ET AL: "CHEMICALLY DERIVED PEPTIDE LIBRARIES: A NEW RESIN AND METHODOLOGY FOR LEAD IDENTIFICATION" INTERNATIONAL JOURNAL OF PEPTIDE AND PROTEIN RESEARCH., vol. 47, no. 1/02, 1 January 1996, COPENHAGEN DK, pages 70-83, XP000545927 * the whole document * -----	1-24	TECHNICAL FIELDS SEARCHED (Int.Cl.6) C07K G01N C12N

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
BERLIN	30 January 1998	De Kok, A

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
Y : particularly relevant if combined with another document of the same category
A : technological background
O : non-written disclosure
P : intermediate document

T : theory or principle underlying the invention
E : earlier patent document, but published on, or after the filing date
D : document cited in the application
L : document cited for other reasons

& : member of the same patent family, corresponding document

EPO FORM 1503 03.82 (P04C01)

PCT WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 7 : G01N 33/68 — A2

(11) International Publication Number: WO 00/63701

(43) International Publication Date: 26 October 2000 (26.10.00)

(21) International Application Number: PCT/US00/10171

(22) International Filing Date: 14 April 2000 (14.04.00)

(30) Priority Data:
60/129,449 15 April 1999 (15.04.99) US

(71) Applicant *(for all designated States except US)*: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY [US/US]; 900 Welch Road, Suite 350, Palo Alto, CA 94304 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: BROWN, Patrick [US/US]; 76 Peter Coutts Circle, Stanford, CA 94305 (US). HAAB, Brian [US/US]; 1922 Grant #1, Berkeley, CA 94703 (US).

(74) Agent: SHERWOOD, Pamela, J.; Bozicevic, Field & Francis LLP, 200 Middlefield Road, Suite 200, Menlo Park, CA 94025 (US).

(81) Designated States: CA, JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

Published
Without international search report and to be republished upon receipt of that report.

(54) Title: MICROARRAYS OF POLYPEPTIDES

(57) Abstract

Microarrays of polypeptides on a solid support are provided. The microarray compositions find use in the multiplexed detection and quantitation of ligands, *e.g.* antigens or antibodies, in a miniaturized format. The substrate is used for detecting binding of ligands to a plurality of polypeptides for screening and diagnostic purposes.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania
AM	Armenia
AT	Austria
AU	Australia
AZ	Azerbaijan
BA	Bosnia and Herzegovina
BB	Barbados
BE	Belgium
BF	Burkina Faso
BG	Bulgaria
BJ	Benin
BR	Brazil
BY	Belarus
CA	Canada
CF	Central African Republic
CG	Congo
CH	Switzerland
CI	Côte d'Ivoire
CM	Cameroon
CN	China
CU	Cuba
CZ	Czech Republic
DE	Germany
DK	Denmark
EE	Estonia
ES	Spain
FI	Finland
FR	France
GA	Gabon
GB	United Kingdom
GE	Georgia
GH	Ghana
GN	Guinea
GR	Greece
HU	Hungary
IE	Ireland
IL	Israel
IS	Iceland
IT	Italy
JP	Japan
KE	Kenya
KG	Kyrgyzstan
KP	Democratic People's Republic of Korea
KR	Republic of Korea
KZ	Kazakstan
LC	Saint Lucia
LI	Liechtenstein
LK	Sri Lanka
LR	Liberia
LS	Lescotho
LT	Lithuania
LU	Luxembourg
LV	Latvia
MC	Monaco
MD	Republic of Moldova
MG	Madagascar
MK	The former Yugoslav Republic of Macedonia
ML	Mali
MN	Mongolia
MR	Mauritania
MW	Malawi
MX	Mexico
NE	Niger
NL	Netherlands
NO	Norway
NZ	New Zealand
PL	Poland
PT	Portugal
RO	Romania
RU	Russian Federation
SD	Sudan
SE	Sweden
SG	Singapore
SI	Slovenia
SK	Slovakia
SN	Senegal
SZ	Swaziland
TD	Chad
TG	Togo
TJ	Tajikistan
TM	Turkmenistan
TR	Turkey
TT	Trinidad and Tobago
UA	Ukraine
UG	Uganda
US	United States of America
UZ	Uzbekistan
VN	Viet Nam
YU	Yugoslavia
ZW	Zimbabwe

MICROARRAYS OF POLYPEPTIDES

FIELD OF THE INVENTION

This invention relates to methods and apparatus for fabricating microarrays of biological samples, and the uses thereof.

BACKGROUND OF THE INVENTION

Life and development of all organisms are determined by molecular interactions, *e.g.* between DNA and proteins, proteins and proteins, or proteins and small molecules. Among these, protein-protein interactions play an especially important role, for example with the interactions between antibodies and antigens, receptors and peptide- or protein-hormones, enzymes and substrates or inhibitors. Many of the best-selling drugs either act by targeting proteins or are proteins. In addition, many molecular markers of disease, which are th basis of diagnostics, are proteins.

The development of techniques and reagents for high throughput protein analysis has been of great interest. In particular, the increasing knowledge of DNA sequence in organisms of interest has spurred interest in protein expression analysis. There is now a rapidly growing awareness of just how important proteomics is to understand and organiz the human genome. Information about the complement of proteins present in a cell is a key to accelerate the discovery of medically important proteins and the genes from which they derive.

Genomics establishes the relationship between gene activity and particular diseases. However most disease processes are manifested not at the level of genes, but at the protein level. There is often a poor correlation between the level of activity of different genes and the relative abundance of the corresponding proteins. Also a protein and its post-translational modifications are not directly encoded for by the same gene, therefore the complete structure of individual proteins cannot be determined by reference to the gene alone.

Assays directed towards protein binding can be used for the quantitation of protein expression; the determination of specific interactions; to determine the presence of ligands for a protein, and the like. Methods of quantitating proteins in a sample by determining binding to a cognate antibody are known in the art.

For example, solid-phase radioimmunoassay (RIA) of antigens or antibodies in a serum sample are well known. Catt *et al.* have reported such techniques on the surface of plastic tubes (U.S. Pat. No. 3,646,346) and plastic discs (J. Lab. & Clin. Med., 70: 820 (1967). In such techniques, an excess of specific antibody is first adsorbed to a support

surface. Then, the sample to be assayed is immunologically reacted with such surface in a sandwich or competitive binding technique. In the competitive binding technique, illustrated in U.S. Pat. No. 3,555,143, the concentration of antigen to be d termined and a known quantity of radioactively tagged antigen are immunologically reacted with the antibody-adsorbed surface. The labeled antigen bound to the antibody on the surface is then quantitated to determine indirectly the total quantity of antigen in the original sample. In the sandwich technique, serum containing an unknown concentration of antigen is immunologically reacted with the antibody-containing surface. Then in a following step, the bound antigen is incubated with labeled antibody and the amount of immunologically bound, labeled antibody is subsequently measured.

The development of high-throughput, parallel systems for protein analysis are of great interest, particularly where the analysis can use small amounts of material for analysis. Preferably such systems provide for the use of complex molecules with high binding affinity for their ligands, such as antibodies, protein receptors, and the like.

Literature:

Publications of interest include: Abouzied, et al., Journal of AOAC International 77(2):495-500 (1994). Bohlander, et al., Genomics 13:1322-1324 (1992). Drmanac, et al., Science 260:1649-1652 (1993). Fodor, et al., Science 251:767-773 (1991). Khrapko, et al., DNA Sequence 1:375-388 (1991). Kuriyama, et al., An Isfet Biosensor, Applied Biosensors (Donald Wise, Ed.), Butterworths, pp. 93-114 (1989). Lehrach, *et al.*, Hybridization Fingerprinting in Genome Mapping And Sequencing, Genome Analysis, Vol 1 (Davies and Tilgham, Eds.), Cold Spring Harbor Press, pp. 39-81 (1990). Maniatis, et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press (1989). Nelson, et al., Nature Genetics 4:11-18 (1993). Pirrung, et al., U.S. Pat. No. 5,143,854 (1992). Riles, et al., Genetics 134:81-150 (1993). Schena, M. et al., Proc. Nat. Acad. Sci. USA 89:3894-3898 (1992). Southern, et al., Genomics 13:1008-1017 (1992).

SUMMARY OF THE INVENTION

Methods are provided for forming a microarray of analyte-assay regions on a solid support, where each region in the array has a known amount of a selected, analyte-specific reagent. The method involves first loading a solution of a selected analyte-specific reagent in a reagent-dispensing device having an elongate capillary channel (i) formed by spaced-apart, coextensive elongate members, (ii) adapted to hold a quantity of the reagent solution and (iii) having a tip region at which aqueous solution in the channel forms a m niscus. The channel is preferably formed by a pair of spaced-apart tapered elements. The microarray

compositions find use in the multiplexed detection and quantitation of ligands, *e.g.* antigens or antibodies, in a miniaturized format.

In another aspect, the invention includes a substrate with a surface having a microarray of at least 10^3 distinct polynucleotide or polypeptide biopolymers in a surface area of less than about 1 cm^2. Each distinct biopolymer is disposed at a separate, defined position in said array, has a length of at least 50 subunits, and is present in a defined amount between about 0.1 femtomoles and 100 nanomoles.

The substrate may be used for detecting binding of ligands to a plurality of different-sequence, immobilized biopolymers. The substrate includes, in one aspect, a glass support, a coating of a polycationic polymer, such as polylysine, on said surface of the support, and an array of distinct biopolymers electrostatically bound non-covalently to said coating, where each distinct biopolymer is disposed at a separate, defined position in a surface array.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a side view of a reagent-dispensing device having a open-capillary dispensing head constructed for use in one embodiment of the invention;

FIGS. 2A-2C illustrate steps in the delivery of a fixed-volume bead on a hydrophobic surface employing the dispensing head from FIG. 1, in accordance with one embodiment of the method of the invention;

FIG. 3 shows a portion of a two-dimensional array of analyte-assay regions constructed according to the method of the invention;

FIG. 4 is a planar view showing components of an automated apparatus for forming arrays in accordance with the invention.

FIG. 5 shows the concentration profiles in a microarray of 110 antigens.

FIG. 6 shows the detection of protein as a ratio of the signal from two fluorochromes, against the dilution of the protein sample.

FIG. 7 shows graphs of the protein quantitation after dilution into serum.

FIG. 8 depicts the combinatorial detection of multiple antibodies.

DETAILED DESCRIPTION OF THE INVENTION

Methods and compositions are provided for forming a microarray of polypeptide regions on a solid support, where each region in the array has a known amount of a selected polypeptide. A robotic printer is used to deposit microdrops of protein solutions onto a derivatized planar surface substrate, where the derivatized surface binds the polypeptide, *e.g.* poly-lysine, and the like. The substrate with a surface having a microarray is spotted at a high density, usually of at least 10^3 distinct polypeptide in a surface area of less than about

1 cm^2. Each distinct polypeptide is present in a defined amount between about 0.1 femtomoles and 100 nanomoles. Any polypeptide can be used, although generally the polypeptide will be at least about 50 amino acids in length.

The microarrays are widely used in quantitative and analytical methods for the detection and quantitation of proteins, or compounds that interact with proteins, such as polynucleotides, hormones, vitamins and other co-factors, *etc.* Typically a sample comprising ligands that are suspected of binding to a polypeptide immobilized on the microarray are added to the microarray under conditions that allow specific binding between the polypeptide and the ligand. The unbound sample is washed from the microarray, and the bound ligand is detected by any suitable method, *e.g.* through the use of detectable labels present on the ligand, or provided in a second, detecting step. Sample consumption is much lower than traditional immunoassays due to the highly parallel and miniaturized format of the present invention. The quantitative measurement of many components in parallel allows diagnosis and recognition of physiological and phenotypic characteristics of a sample to be based on a multidimensional pattern of expression, rather than simply a few parameters.

In one embodiment of the invention, comparative fluorescence is used to monitor the presence of bound ligands to the microarray. The use of comparative fluorescence measurements allows greater precision across a wide range of ligand concentrations and binding affinities, as compared to methods that measure the absolute amount of bound ligand.

In one embodiment of the invention, the biopolymers are polypeptides, *e.g.* antigens, antibodies, receptors, *etc.*, that have functional binding properties imparted by the three-dimensional structure of the polypeptide, which structure is frequently dependent on contacts made between non-contiguous amino acid residues, such as disulphide bonds between cysteine residues, hydrophobic pockets, and the like. Such binding properties include the specific binding between a protein receptor and one or more of its naturally occurring ligands, for example cytokines and cytokine receptors, hormones and hormone receptors, chemokines and chemokine receptors, *etc.*, including a range of protein and polypeptide molecules that provide for specific interactions within a biological system. DNA binding proteins, *e.g.* nuclear hormone receptors; transcription factors, *etc.* may be provided on a microarray, where the proteins retain the ability to specifically define their cognate DNA motif. Microarrays that maintain binding properties of antigen specific immunological receptors are of particular interest, which receptors include antibodies, T cell antigen r ceptors, and major histocompatibility complex proteins.

These and other objects and features of the invention will become more fully apparent when the following detailed description of the invention is read in conjunction with the accompanying figures.

Definitions

Unless indicated otherwise, the terms defined below have the following meanings:

"*Ligand*" refers to one member of a ligand/anti-ligand binding pair. The ligand may be, for example, one of the nucleic acid strands in a complementary, hybridized nucleic acid duplex binding pair; an effector molecule in an effector/receptor binding pair; or an antigen in an antigen/antibody or antigen/antibody fragment binding pair.

"*Anti-ligand*" refers to the opposite member of a ligand/anti-ligand binding pair. The anti-ligand may be the other of the nucleic acid strands in a complementary, hybridized nucleic acid duplex binding pair; the receptor molecule in an effector/receptor binding pair; or an antibody or antibody fragment molecule in antigen/antibody or antigen/antibody fragment binding pair, respectively.

"*Analyte*" or "*analyte molecule*" refers to a molecule, typically a macromolecule, such as a polynucleotide or polypeptide, whose presence, amount, and/or identity are to be determined. The analyte is one member of a ligand/anti-ligand pair.

"*Analyte-specific assay reagent*" refers to a molecule effective to bind specifically to an analyte molecule. The reagent is the opposite member of a ligand/anti-ligand binding pair.

An "*array of regions on a solid support*" is a linear or two-dimensional array of preferably discrete regions, each having a finite area, formed on the surface of a solid support.

A "*microarray*" is an array of regions having a density of discrete regions of at least about 100/cm^2, and preferably at least about 1000/cm^2. The regions in a microarray have typical dimensions, *e.g.*, diameters, in the range of between about 10-250 μm, and are separated from other regions in the array by about the same distance.

A support surface is "*hydrophobic*" if a aqueous-medium droplet applied to the surface does not spread out substantially beyond the area size of the applied droplet. That is, the surface acts to prevent spreading of the droplet applied to the surface by hydrophobic interaction with the droplet.

A "*meniscus*" means a concave or convex surface that forms on the bottom of a liquid in a channel as a result of the surface tension of the liquid.

"*Distinct biopolymers*", as applied to the biopolymers forming a microarray, means an array member which is distinct from other array members on the basis of a different biopolymer sequence, and/or different concentrations of the same or distinct biopolymers,

and/or different mixtures of distinct or different-concentration biopolymers. Thus an array of "distinct polynucleotides" means an array containing, as its members, (i) distinct polynucleotides, which may have a defined amount in each member, (ii) different, graded concentrations of given-sequence polynucleotides, and/or (iii) different-composition mixtures of two or more distinct polynucleotides.

"*Cell type*" means a cell from a given source, e.g., a tissue, or organ, or a cell in a given state of differentiation, or a cell associated with a given pathology or genetic makeup.

Method of Microarray Formation

This section describes a method of forming a microarray of analyte-assay regions on a solid support or substrate, where each region in the array has a known amount of a selected, analyte-specific reagent.

FIG. 1 illustrates, in a partially schematic view, a reagent-dispensing device 10 useful in practicing the method. The device generally includes a reagent dispenser 12 having an elongate open capillary channel 14 adapted to hold a quantity of the reagent solution, such as indicated at 16, as will be described below. The capillary channel is formed by a pair of spaced-apart, coextensive, elongate members 12a, 12b which are tapered toward one another and converge at a tip or tip region 18 at the lower end of the channel. More generally, the open channel is formed by at least two elongate, spaced-apart members adapted to hold a quantity of reagent solutions and having a tip region at which aqueous solution in the channel forms a meniscus, such as the concave meniscus illustrated at 20 in FIG. 2A. The advantages of the open channel construction of the dispenser are discussed below.

With continued reference to FIG. 1, the dispenser device also includes structure for moving the dispenser rapidly toward and away from a support surface, for effecting deposition of a known amount of solution in the dispenser on a support, as will be described below with reference to FIGS. 2A-2C. In the embodiment shown, this structure includes a solenoid 22 which is activatable to draw a solenoid piston 24 rapidly downwardly, then release the piston, e.g., under spring bias, to a normal, raised position, as shown. The dispenser is carried on the piston by a connecting member 26, as shown. The just-described moving structure is also referred to herein as dispensing means for moving the dispenser into engagement with a solid support, for dispensing a known volume of fluid on the support.

The dispensing device just described is carried on an arm 28 that may be moved either linearly or in an x-y plane to position the disp nser at a selected deposition position, as will be described.

FIGS. 2A-2C illustrate the method of depositing a known amount of reagent solution in the just-described dispenser on the surface of a solid support, such as the support indicated at 30. The support is a polymer, glass, or other solid-material support having a surface indicated at 31.

In one general embodiment, the surface is a relatively hydrophilic, i.e., wettable surface, such as a surface having native, bound or covalently attached charged groups. One such surface described below is a glass surface having an absorbed layer of a polycationic polymer, such as poly-l-lysine.

In another embodiment, the surface has or is formed to have a relatively hydrophobic character, i.e., one that causes aqueous medium deposited on the surface to bead. A variety of known hydrophobic polymers, such as polystyrene, polypropylene, or polyethylene have desired hydrophobic properties, as do glass and a variety of lubricant or other hydrophobic films that may be applied to the support surface.

Initially, the dispenser is loaded with a selected analyte-specific reagent solution, such as by dipping the dispenser tip, after washing, into a solution of the reagent, and allowing filling by capillary flow into the dispenser channel. The dispenser is now moved to a selected position with respect to a support surface, placing the dispenser tip directly above the support-surface position at which the reagent is to be deposited. This movement takes place with the dispenser tip in its raised position, as seen in FIG. 2A, where the tip is typically at least several 1-5 mm above the surface of the substrate.

With the dispenser so positioned, solenoid 22 is now activated to cause the dispenser tip to move rapidly toward and away from the substrate surface, making momentary contact with the surface, in effect, tapping the tip of the dispenser against the support surface. The tapping movement of the tip against the surface acts to break the liquid meniscus in the tip channel, bringing the liquid in the tip into contact with the support surface. This, in turn, produces a flowing of the liquid into the capillary space between the tip and the surface, acting to draw liquid out of the dispenser channel, as seen in FIG. 2B.

FIG. 2C shows flow of fluid from the tip onto the support surface, which in this case is a hydrophobic surface. The figure illustrates that liquid continues to flow from the dispenser onto the support surface until it forms a liquid bead 32. At a given bead size, i.e., volume, the tendency of liquid to flow onto the surface will be balanced by the hydrophobic surface interaction of the bead with the support surface, which acts to limit the total bead area on the surface, and by the surface tension of the droplet, which tends toward a given bead curvature. At this point, a given bead volume will have formed, and continued contact of the dispenser tip with the bead, as the dispenser tip is being withdrawn, will have little or no effect on bead volume.

For liquid-dispensing on a more hydrophilic surface, the liquid will have less of a tendency to bead, and the dispensed volume will be more sensitive to the total dwell time of the dispenser tip in the immediate vicinity of the support surfac , e.g., the positions illustrated in FIGS. 2B and 2C.

The desired deposition volume, i.e., bead volume, formed by this method is preferably in the range 2 pl (picoliters) to 2 nl (nanoliters), although volumes as high as 100 nl or more may be dispensed. It will be appreciated that the selected dispensed volume will depend on (i) the "footprint" of the dispenser tip, i.e., the size of the area spanned by the tip, (ii) the hydrophobicity of the support surface, and (iii) the time of contact with and rate of withdrawal of the tip from the support surface. In addition, bead size may be reduced by increasing the viscosity of the medium, effectively reducing the flow time of liquid from the dispenser onto the support surface. The drop size may be further constrained by depositing the drop in a hydrophilic region surrounded by a hydrophobic grid pattern on the support surface.

In a typical embodiment, the dispenser tip is tapped rapidly against the support surface, with a total residence time in contact with the support of less than about 1 msec, and a rate of upward travel from the surface of about 10 cm/sec.

Assuming that the bead that forms on contact with the surface is a hemispherical bead, with a diameter approximately equal to the width of the dispenser tip, as shown in FIG. 2C, the volume of the bead formed in relation to dispenser tip width (d) is given in Table 1 below. As seen, the volume of the bead ranges between 2 pl to 2 nl as the width size is increased from about 20 to 200 μm.

TABLE 1

d	Volume (nl)
20 μm	2×10^{-3}
50 μm	3.1×10^{-2}
100 μm	2.5×10^{-1}
200 μ	2

At a given tip size, bead volume can be reduced in a controlled fashion by increasing surface hydrophobicity, reducing time of contact of the tip with the surface, increasing rate of movement of the tip away from the surface, and/or increasing the viscosity of the medium. Once these parameters are fixed, a selected deposition volume in the desired pl to nl rang can be achieved in a repeatable fashion.

After depositing a bead at one selected location on a support, the tip is typically moved to a corresponding position on a second support, a droplet is deposited at that position, and this process is repeated until a liquid droplet of the reagent has been deposited at a selected position on each of a plurality of supports.

The tip is then washed to remove the reagent liquid, filled with another reagent liquid and this reagent is now deposited at each another array position on each of the supports. In one embodiment, the tip is washed and refilled by the steps of (i) dipping the capillary channel of the device in a wash solution, (ii) removing wash solution drawn into the capillary channel, and (iii) dipping the capillary channel into the new reagent solution.

From the foregoing, it will be appreciated that the tweezers-like, open-capillary dispenser tip provides the advantages that (i) the open channel of the tip facilitates rapid, efficient washing and drying before reloading the tip with a new reagent, (ii) passive capillary action can load the sample directly from a standard microwell plate while retaining sufficient sample in the open capillary reservoir for the printing of numerous arrays, (iii) open capillaries are less prone to clogging than closed capillaries, and (iv) open capillaries do not require a perfectly faced bottom surface for fluid delivery.

A portion of a microarray 36 formed on the surface 38 of a solid support 40 in accordance with the method just described is shown in FIG. 3. The array is formed of a plurality of analyte-specific reagent regions, such as regions 42, where each region may include a different analyte-specific reagent. As indicated above, the diameter of each region is preferably between about 20-200 μm. The spacing between each region and its closest (non-diagonal) neighbor, measured from center-to-center (indicated at 44), is preferably in the range of about 20-400 μm. Thus, for example, an array having a center-to-center spacing of about 250 μm contains about 40 regions/cm or 1,600 regions/cm^2. After formation of the array, the support is treated to evaporate the liquid of the droplet forming each region, to leave a desired array of dried, relatively flat regions. This drying may be done by heating or under vacuum.

In some cases, it is desired to first rehydrate the droplets containing the analyte reagents to allow for more time for adsorption to the solid support. It is also possible to spot out the analyte reagents in a humid environment so that droplets do not dry until the arraying operation is complete.

Automated Apparatus for Forming Arrays

In another aspect, the invention includes an automated apparatus for forming an array of analyte-assay regions on a solid support, where each region in the array has a known amount of a selected, analyte-specific reagent.

The apparatus is shown in planar, and partially schematic vi w in FIG. 4. A dispens r device 72 in the apparatus has the basic construction described above with respect to FIG. 1, and includes a dispenser 74 having an open-capillary channel terminating at a tip, substantially as shown in FIGS. 1 and 2A-2C.

The dispenser is mounted in the device for movement toward and away from a dispensing position at which the tip of the dispenser taps a support surface, to dispense a selected volume of reagent solution, as described above. This movement is effected by a solenoid 76 as described above. Solenoid 76 is under the control of a control unit 77 whose operation will be described below. The solenoid is also referred to herein as dispensing means for moving the device into tapping engagement with a support, when the device is positioned at a defined array position with respect to that support.

The dispenser device is carried on an arm 74 which is threadedly mounted on a worm screw 80 driven (rotated) in a desired direction by a stepper motor 82 also under the control of unit 77. At its left end in the figure screw 80 is carried in a sleeve 84 for rotation about the screw axis. At its other end, the screw is mounted to the drive shaft of the stepper motor, which in turn is carried on a sleeve 86. The dispenser device, worm screw, the two sleeves mounting the worm screw, and the stepper motor used in moving the device in the "x" (horizontal) direction in the figure form what is referred to here collectively as a displacement assembly 86.

The displacement assembly is constructed to produce precise, micro-range movement in the direction of the screw, i.e., along an x axis in the figure. In one mode, the assembly functions to move the dispenser in x-axis increments having a selected distance in the range 5-25 μm. In another mode, the dispenser unit may be moved in precise x-axis increments of several microns or more, for positioning the dispenser at associated positions on adjacent supports, as will be described below.

The displacement assembly, in turn, is mounted for movement in the "y" (vertical) axis of the figure, for positioning the dispenser at a selected y axis position. The structure mounting the assembly includes a fixed rod 88 mounted rigidly between a pair of frame bars 90, 92, and a worm screw 94 mounted for rotation between a pair of frame bars 96, 98. The worm screw is driven (rotated) by a stepper motor 100 which operates under the control of unit 77. The motor is mounted on bar 96, as shown.

The structure just described, including worm screw 94 and motor 100, is constructed to produce precise, micro-range movement in the direction of the screw, i.e., along a y axis in the figure. As above, the structure functions in one mode to move the dispenser in y-axis increments having a selected distance in the range 5-250 μm, and in a second mode, to

move the dispenser in precise y-axis increments of several microns (μm) or mor , for positioning the dispenser at associated positions on adjacent supports.

The displacement assembly and structure for moving this assembly in the y axis are referred to herein collectively as positioning means for positioning the dispensing device at a selected array position with respect to a support.

A holder 102 in the apparatus functions to hold a plurality of supports, such as supports 104 on which the microarrays of reagent regions are to be formed by th apparatus. The holder provides a number of recessed slots, such as slot 106, which receive the supports, and position them at precise selected positions with respect to the frame bars on which the dispenser moving means is mounted.

As noted above, the control unit in the device functions to actuate the two stepper motors and dispenser solenoid in a sequence designed for automated operation of the apparatus in forming a selected microarray of reagent regions on each of a plurality of supports.

The control unit is constructed, according to conventional microprocessor control principles, to provide appropriate signals to each of the solenoid and each of the stepper motors, in a given timed sequence and for appropriate signaling time. The construction of the unit, and the settings that are selected by the user to achieve a desired array pattern, will be understood from the following description of a typical apparatus operation.

Initially, one or more supports are placed in one or more slots in the holder. The dispenser is then moved to a position directly above a well (not shown) containing a solution of the first reagent to be dispensed on the support(s). The dispenser solenoid is actuated now to lower the dispenser tip into this well, causing the capillary channel in the dispenser to fill. Motors 82, 100 are now actuated to position the dispenser at a selected array position at the first of the supports. Solenoid actuation of the dispenser is then effective to dispense a selected-volume droplet of that reagent at this location. As noted above, this operation is effective to dispense a selected volume preferably between 2 pl and 2 nl of the reagent solution.

The dispenser is now moved to the corresponding position at an adjacent support and a similar volume of the solution is dispensed at this position. The process is repeated until the reagent has been dispensed at this preselected corresponding position on each of the supports.

Where it is desired to dispense a single reagent at more than two array positions on a support, the dispenser may be moved to different array positions at each support, before moving the dispenser to a new support, or solution can be dispensed at individual positions

on each support, at one selected position, then the cycle repeated for each new array position.

To dispense the next reagent, the dispenser is positioned over a wash solution (not shown), and the dispenser tip is dipped in and out of this solution until the reagent solution has been substantially washed from the tip. Solution can be removed from the tip, after each dipping, by vacuum, compressed air spray, sponge, or the like.

The dispenser tip is now dipped in a second reagent well, and the filled tip is moved to a second selected array position in the first support. The process of dispensing reagent at each of the corresponding second-array positions is then carried out as above. This process is repeated until an entire microarray of reagent solutions on each of the supports has been formed.

Microarray Substrate

This section describes embodiments of a substrate having a microarray of biological polymers carried on the substrate surface, in particular a microarray of distinct polypeptides bound on a glass slide coated with a polycationic polymer is described.

A substrate is formed according to another aspect of the invention, and intended for use in detecting binding of labeled ligands to one or more of a plurality distinct biopolymers. In one embodiment, the substrate includes a glass substrate having formed on its surface, a coating of a polycationic polymer, preferably a cationic polypeptide, such as poly-lysine or poly-arginine. Formed on the polycationic coating is a microarray of distinct biopolymers, each localized at known selected array regions, such as regions.

The slide may be coated by placing a uniform-thickness film of a polycationic polymer, e.g., poly-l-lysine, on the surface of a slide and drying the film to form a dried coating. The amount of polycationic polymer added is sufficient to form at least a monolayer of polymers on the glass surface. The polymer film is bound to surface via electrostatic binding between negative silyl-OH groups on the surface and charged amine groups in the polymers. Poly-l-lysine coated glass slides may be obtained commercially, e.g., from Sigma Chemical Co. (St. Louis, Mo.).

A suitable microarray substrate is also made through chemical derivatization of glass. Silane compounds with appropriate leaving groups on a terminal Si will covalently bond to glass surfaces. A derivatization molecule can be designed to confer the desired chemistry to the surface of the glass substrate. An example of such a bifunctional reagent is amino-propyl-tri(ethoxy)silane, which reacts with glass surfaces at the tri(ethoxy)silane portion of th molecule while leaving the amino portion of the molecule fre . Surfaces having t rminal amino groups are suitable for adsorption of biopolymers in the sam manner as poly-lysine

coated slides. The identity of the terminal surface group can be modified by further chemical reaction. For example, reaction of the terminal amine in the above example with glutaraldehyde results in a terminal aldehyde group. Further layers of modification may be applied to achieve the desired reactivity before spotting the microarray, such as by application of a Protein A or Protein G solution to the silynated glass. Additional surfaces that bind polypeptides are nitrocellulose-coated glass slides, available commercially from Schleicher and Schuell, and protein-binding plastics such as polystyrene.

The spotted polypeptides may be attached by either adsorption or covalent bonding. Adsorption occurs through electrostatic, hydrophobic, Van der Waals, or hydrogen-bonding interactions between the spotted polypeptide and the array substrate. Simple application of the polypeptide solution to the surface in an aqueous environment is sufficient to adsorb the polypeptide. Covalent attachment is achieved by reaction of functional groups on the polypeptide with a chemically activated surface. For example, if the surface has been activated with a highly reactive electrophilic group such as an aldehyde or succinimide group, unmodified polypeptides react at amine groups, as at lysine residues or the terminal amine, to form a covalent bond.

To form the microarray, defined volumes of distinct biopolymers are deposited on the polymer-coated slide, as described in Section II. According to an important feature of the substrate, the deposited biopolymers remain bound to the coated slide surface non-covalently when an aqueous sample is applied to the substrate under conditions that allow binding of labeled ligands in the sample to cognate binding partners in the substrate array.

In a preferred embodiment, each microarray contains at least 10^3 distinct polynucleotide or polypeptide biopolymers per surface area of less than about 1 cm^2. In one embodiment, the microarray contains 400 regions in an area of about 16 mm^2, or 2.5 x 10^3 regions/cm^2. Also in a preferred embodiment, the biopolymers in each microarray region are present in a defined amount between about 0.1 femtomoles and 100 nanomoles (in the case of polynucleotides). As above, the ability to form high-density arrays of this type, where each region is formed of a well-defined amount of deposited material, can be achieved in accordance with the microarray-forming method described in Section II.

Also in a preferred embodiment, the biopolymers have lengths of at least about 50 units, *e.g.* amino acids, nucleotides, *etc.*, i.e., substantially longer than polymers which can be formed in high-density arrays by various *in situ* synthesis schemes.

The polypeptide biopolymers may comprise polypeptides from any source. Polypeptides of interest include those isolated from cells or other biological sources, synthesized polypeptides, including synthesized peptides and peptides selected from combinatorial libraries, polypeptides synthesized from recombinant nucleic acids, and the

like. In one embodiment, the polypeptides are isolated from phage display libraries or clones (see Huse et al. (1989) Science. 1989 246(4935):1275-81; Winter t al. (1994) Annu Rev Immunol. 12:433-55; Clackson et al. (1991) Nature 352(6336):624-8). Usually the polypeptides on each discrete region of the array will be substantially pure.

Uses of the Microarrays

Arrays of whole cells, peptides, enzymes, antibodies, antigens, receptors, ligands, phospholipids, polymers, drug congener preparations or chemical substances can be fabricated by the means described in this invention for large scale screening assays in medical diagnostics, drug discovery, molecular biology, immunology and toxicology.

Microarrays of immobilized polypeptides prepared in accordance with the invention can be used for large scale binding assays in numerous diagnostic and screening applications. The multiplexed measurement of quantitative variation in levels of large numbers of proteins allows the recognition of patterns defined by several to many different proteins. One can simultaneously assess many physiological parameters and disease-specific patterns.

One embodiment of the invention involves the separation, identification and characterization of proteins present in a biological sample. For example, by comparison of disease and control samples, it is possible to identify "disease specific proteins". These proteins may be used as targets for drug development or as molecular markers of disease.

Polypeptide arrays are used to monitor the expression levels of proteins in a sample where such samples may include biopsy of a tissue of interest, cultured cells, microbial cell populations, biological fluids, including blood, plasma, lymph, synovial fluid, cerebrospinal fluid, cell lysates, culture supernatants, amniotic fluid, *etc.*, and derivatives thereof. Of particular interest are clinical samples of biological fluids, including blood and derivatives thereof, cerebrospinal fluid, urine, saliva, lymph, synovial fluids, *etc.* Such measurements may be quantitative, semi-quantitative, or qualitative. Where the assay is to be quantitative or semi-quantitative, it will preferably comprise a competition-type format, for example between labeled and unlabeled samples, or between samples that are differentially labeled.

Assays to detect the presence of ligands to the immobilized polypeptides may be performed as follows, although the methods need not be limited to those set forth herein.

Samples, fractions or aliquots thereof are added to a microarray comprising bound polypeptide. Samples may comprise a wide variety of biological fluids or extracts as described above. Preferably, a series of standards, containing known concentrations of control ligand(s) is assayed in parallel with the samples or aliquots thereof to s rv as

controls. The incubation time should be sufficient for ligand molecules to bind the polypeptides. Generally, from about 0.1 to 3 hr is sufficient, usually 1 hr sufficing.

After incubation, the insoluble support is generally washed of non-bound components. Generally, a dilute non-ionic detergent medium at an appropriate pH, generally 7-8, is used as a wash medium. From one to six washes may be employed, with sufficient volume to thoroughly wash non-specifically bound proteins present in the sample.

In order to detect the presence of bound ligands, a variety of methods may be used. These fall into three general groups. The ligand itself may be labeled with a detectable label, and the amount of bound label directly measured. Alternatively, the labeled sample may be mixed with a differentially labeled, or unlabeled sample in a competition assay. In yet another embodiment, the sample itself is not labeled, but a second stage labeled reagent is added in order to quantitate the amount of ligand present.

Examples of labels that permit direct measurement of ligand binding include radiolabels, such as ^{3}H or ^{125}I, fluorescers, dyes, beads, chemilumninescers, colloidal particles, and the like. Suitable fluorescent dyes are known in the art, including fluorescein isothiocyanate (FITC); rhodamine and rhodamine derivatives; Texas Red; phycoerythrin; allophycocyanin; 6-carboxyfluorescein (6-FAM); 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein (JOE); 6-carboxy-X-rhodamine (ROX); 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX); 5-carboxyfluorescein (5-FAM); N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA); sulfonated rhodamine; Cy3; Cy5; *etc.* Preferably the compound to be labeled is combined with an activated dye that reacts with a group present on the ligand, e.g. amine groups, thiol groups, aldehyde groups, *etc.*

Particularly where a second stage detection is performed, for example by the addition of labeled antibodies that recognize the ligand, the label can be a covalently bound enzyme capable of providing a detectable product signal after addition of suitable substrate. Examples of suitable enzymes for use in conjugates include horseradish peroxidase, alkaline phosphatase, malate dehydrogenase and the like. Where not commercially available, such antibody-enzyme conjugates are readily produced by techniques known to those skilled in the art. The second stage binding reagent may be any compound that binds the ligands with sufficient specificity such that it can be distinguished from other components present. In a preferred embodiment, second stage binding reagents are antibodies specific for the ligand, either monoclonal or polyclonal sera, *e.g.* mouse anti-human antibodies, *etc.*

For an amplification of signal, the ligand may be labeled with an agent such as biotin, digoxigenin, *etc.*, where the second stage reagent will comprise avidin, streptavidin, anti-digoxigenin antibodies, *etc.* as appropriate for the label.

Microarrays can be scanned to detect binding of the ligands, *e.g.* by using a scanning laser microscope, by fluorimetry, a modified ELISA plate reader, *tc.* For example, a scanning laser microscope may perform a separate scan, using the appropriate excitation line, for each of the fluorophores used. The digital images generated from the scan are then combined for subsequent analysis. For any particular array element, the ratio of the fluorescent signal with one label is compared to the fluorescent signal from the other label DNA, and the relative abundance determined.

The microarrays and methods of detecting ligands may be used for a number of screening, investigative and diagnostic assays. In one application, an array of antibodies is bound to total protein from an organism to monitor protein expression for research or diagnostic purposes. Labeling total protein from a normal cell with one color fluorophore and total protein from a diseased cell with another color fluorophore and simultaneously binding the two samples to the same array allows for differential protein expression to be measured as the ratio of the two fluorophore intensities. This two-color experiment can be used to monitor expression in different tissue types, disease states, response to drugs, or response to environmental factors.

In screening assays, for example to determine whether a protein or proteins are implicated in a disease pathway or are correlated with a disease-specific phenotype, measurements may be made from cultured cells. Such cells may be experimentally manipulated by the addition of pharmacologically active agents that act on a target or pathway of interest. This application is important for elucidation of biological function or discovery of therapeutic targets.

For many diagnostic and investigative purposes it is useful to measurement levels of ligands, *e.g.* protein ligands, in blood or serum. This application is important for the discovery and diagnosis of clinically useful markers that correlate with a particular diagnosis or prognosis. For example, by monitoring a range of antibody or T cell receptor specificities in parallel, one may determine the levels and kinetics of antibodies during the course of autoimmune disease, during infection, through graft rejection, *etc.* Alternatively, novel protein markers associated with a disease of interest may be developed through comparisons of normal and diseased blood sample, or by comparing clinical samples at different stages of disease.

In another embodiment of the invention, the polypeptide arrays are used to detect post-translational modifications in proteins, which is important in studying signaling pathways and cellular regulation. Post-translational modifications can be detected using antibodies specific for a particular state of a protein, such as phosphorylated, glycosylated, farnesylat d, *etc.*

The detection of these interactions between ligands and polypeptides can lead to a medical diagnosis. For example, the identity of a pathogenic microorganism can be established unambiguously by binding a sample of the unknown pathogen to an array containing many types of antibodies specific for known pathogenic antigens.

EXPERIMENTAL

It is to be understood that this invention is not limited to the particular methodology, protocols, cell lines, animal species or genera, and reagents described, as such may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

As used herein the singular forms "a", "and", and "the" include plural referents unless the context clearly dictates otherwise. All technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs unless clearly indicated otherwise.

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the subject invention, and are not intended to limit the scope of what is regarded as the invention. Efforts have been made to ensure accuracy with respect to the numbers used (*e.g.* amounts, temperature, concentrations, *etc.*) but some experimental errors and deviations should be allowed for. Unless otherwise indicated, parts are parts by weight, molecular weight is average molecular weight, temperature is in degrees centigrade; and pressure is at or near atmospheric.

EXAMPLE 1

Antibody and Antigen Microarrays

A set of antibody and antigen pairs with which highly controlled experiments could be performed was assembled, using 115 different ligand/anti-ligand pairs.

Methods

Array preparation: Antibody solutions were prepared at 100-200 µg/mL in a PBS/0.02% sodium azide buffer without glycerol. The antibodies were spotted onto glass slides treated with poly-l-lysine. The slides are derivitized by the following procedure. Place slides in slide racks, then racks in chambers. Prepare cleaning solution by dissolving 70 g NaOH in 280 mL ddH2O, then adding 420 mL 95% ethanol. Total volume is 700 mL (= 2 X 350 mL); stir until completely mixed. Pour solution into chambers with slides; cover

chambers with glass lids. Mix on orbital shaker for 2 hr. Quickly transfer racks to fr sh chambers filled with ddH2O. Rinse vigorously by plunging racks up and down. Repeat rinses 4X with fresh ddH2O each time. Prepare polylysine solution: 70 mL poly-L-lysine + 70 mL tissue culture PBS in 560 mL water. Transfer slides to polylysine solution and shake 15 min. - 1 hr. Transfer rack to fresh chambers filled with ddH2O. Plunge up and down 5X to rinse. Centrifuge slides on microtiter plate carriers for 5 min. @ 500 rpm. Dry slide racks in 45° C vacuum oven for 10 min.

The antibodies and antigens were prepared in a 384-well microtitre plate containing at least three wells each of 110 different antibodies or antigens. A 16-tip print head on the arrayer spotted the plate three times for a total of 1152 spots, with 9-12 duplicate spots per antibody or antigen. The spacing between spots was 375 micrometers. The arrays were sealed in an airtight container. They can be stored at 4° C for short term storage (~1 month) or frozen for longer storage.

The back sides of the slides were marked with a diamond scribe or indelible marker to delineate the location of the spots. To remove unbound protein, the arrays were dunked several times in PBS/3% non-fat milk/0.1% Tween-20, and transferred immediately to a solution of PBS/3% non-fat milk, and let block overnight at 4° C. The milk solution was first centrifuged (10 minutes at 10000 x g) to remove particulate matter.

After blocking, the slides were dunked and thoroughly agitateed for one minute each in three consecutive room temperature washes of 0.2X PBS to remove the unbound milk protein. The arrays remained in the last wash until application of the protein mixture.

Sample preparation: Protein solutions were prepared in a 0.1 carbonate or phosphate buffer at pH 8.0, using up to ~15 μg protein per array (when using 25 μL per array) at a concentration such that after mixing with the dye solution (see below), the final protein concentration is 0.2-2 mg/mL.

NHS-ester activated Cy-dyes (Amersham, catalog # PA23001 (Cy3) and PA25001 (Cy5)) were dissolved in a 0.1 M pH 8.0 carbonate buffer so that the final concentration of the dye after mixing with the protein solution was 100-300 μM. (Each vial of dye contains 200 nmols.) The dye and protein solutions were mixed, and allowed to react in the dark at room temperature for 45 minutes. The reference protein solution was mixed with the Cy3 dye solution, and the test protein solution with the Cy5 dye solution. The reactions wer quenched by adding enough 1 M pH 8 tris or glycine to each so that at least a 200-fold excess of quencher:dye concentration was achieved.

Each mix was loaded into a microconcentrator having the appropriate molecular weight cutoff. A 3000 D cutoff captures most proteins while still removing the dye. If smaller

proteins are not important, the 10000 D cutoff is faster. The mix was centrifuged according to the microconcentrator instructions. The 10000 D microcon typically requires 20 minutes and the 3000 D microcon requires 80 minutes of centrifugation at 10000 x g and room temperature. After centrifuging, 3% milk blocker was added to either the Cy5 or Cy3-labeled protein mixes. (The milk must first be centrifuged to remove particulate matter: 10 minutes at 10000 x g.) Add 25 μL milk for each array to be generated from the protein mix. PBS was added to each microcon to a 500 μL volume, and centrifuged again. The concentrated samples were collected into a small volume (~5 μL) of PBS to prevent drying and precipitation.

The Cy3-labeled reference protein solution was distributed to the appropriate Cy5-labeled test protein solutions, and PBS added to each mix to achieve a volume of 25 μL per array. Particulate matter or precipitate was removed by 1) filtering with a 0.45 μm spin filter, or 2) centrifuging 10 minutes at 14000 x g and pipetting out the supernatant.

Detection: Each array was removed individually from the PBS wash. Without allowing the array to dry, 25 μL of the dye-labeled protein solution was placed over the spots (within the marked boundaries), with a cover slip placed over the protein solution. The cover slip has dimensions at least ¼ inch longer than the dimensions of the array. The arrays were placed in a sealed humidification chamber with a layer of PBS under the arrays, and incubated at 4° C for approximately two hours. Each array was briefly dunked in PBS to remove the protein solution and the cover slip, and transfered immediately to a slide rack in a PBS/0.1% Tween-20 solution. After all the arrays have been racked in the PBS/Tween solution, they were washed on an orbital shaker for ~20 minutes at room temperature. The arrays were transferred to a new rack (to minimize Tween carryover) in a PBS solution and rocked gently for 5-10 minutes, then transferred to wash solutions of PBS, H_2O, and H_2O for five minutes each of gentle agitation. The arrays were then spin-dried and scanned.

Analysis: The fluorescence intensity at each spot reflects the level of binding to that particular protein. The relative concentration between proteins in differentially dye-labeled pools is determined by comparing the fluorescence intensities between the color channels at each spot. The following method is used to determine relative concentrations.

The location of each analyte spot on the array is outlined using "gridding" software, such as GenePix or ScanAlyze, which places a boundary around each spot on the array.

The fluorescence signal from each spot is determined as the average or median of the pixel intensities within the boundary outlined using the gridding software. Each color channel is treated independently. Optionally statistical methods are used to reject "outlier"

pixels within the circle, i.e. pixels that have intensities significantly outside the average pixel intensity.

The background is subtracted from the signal. The background may be determined as 1) the median or average of pixel intensities from the local area around each spot, or as 2) the median or average or pixel intensities from within certain spots or areas determined to be non-binding background areas. Statistical methods may be used to reject outlier pixels in the background.

The relative binding at each spot between proteins in the separately labeled pools is equivalent to the ratio of fluorescence intensities in the two color channels. In order for the ratio to reflect the true relative concentrations, the background-subtracted signal from one of the color channels must be multiplied by a normalization factor. The normalization factor may be determined by selecting spots for which the true concentrations are known and calculating the factor that most accurately returns the true color ratio. Alternatively, if no control spots are used, one may assume that the average binding across every spot on the array is roughly equal for the two protein pools. A normalization factor is then calculated that gives an average color ratio of one for all the spots on the array.

Once all arrays have been normalized and color ratios have calculated, changes in protein concentration from array to array may be compared. Interpretation is simplest if the same reference pool is used for each experiment.

Results:

To test the specificity, quantitation, and limits of detection of the protein array, six mixes of antigens were made in which the concentration of each protein varied uniquely across the mixes. For example, one protein changed from high to low concentration, another from low to high, and another from low to high to low. The concentrations varied three orders of magnitude over the whole set. This set of six mixes was detected at various concentrations and in various levels of fetal calf serum (FCS) background. The ability to reconstruct the actual concentration changes from the data indicated the level of performance of the microarrays.

Microarrays were constructed containing 6 to 9 duplicate spots from each antibody. Figure 5 presents a series of these arrays generated from the set of six unique protein mixes (labeled with the red-fluorescing dye Cy5) compared against a reference mix (labeled with the green-fluorescing dye Cy3) containing an equal amount of each protein. For each spot on the array, the red/green ratio was calculated and then plotted as a function of dilution. Figure 6 presents plots of the log of the red-to-green ratio (R/G) versus dilution for eight of the antigens. The ideal slope, calculated as the log of the concentration ratio of the proteins,

is shown as a straight solid line decreasing from 1.5 to –1.5. The other lines on the graph represent duplicate spots on the array. The slopes of the experimental data are very similar to the ideal slope over the six concentrations tested, indicating that these antibodies detected the cognate antigens specifically and quantitatively. Deviations from ideal slop appear to occur systematically between the duplicate spots, suggesting that the largest error in quantitation occurred in pipetting or data reduction rather than in random variability in the system.

The detection of a specific protein is limited not only by concentration, but also by the concentration of background proteins. To determine how well specific proteins can be detected in high protein background, the set of unique protein mixes was spiked into varying amounts of FCS before dye labeling. FCS concentrations 10 times greater and 100 times greater than the antigen mix concentration were used. Figure 7 shows the effect of protein background on quantitation for the proteins IgG and flag. Without the serum background, accurate quantitation is observed for both proteins over the entire concentration range, which was from 120 ng/mL to 120 pg/mL. At the 10x serum concentration, the flag protein still shows accurate quantitation, but IgG shows slight deviation from the ideal slope at the high and low limits. At the 100x serum concentration, both proteins exhibit marked deviations from the ideal slope. The partial concentrations (the antigen concentration divided by the total protein concentration) ranged from 4×10^{-5} to 4×10^{-8} for the 100x serum trial. Thus the partial concentration detection limit is ~2×10^{-6} for flag and ~2×10^{-7} for IgG using these antibodies. These partial concentrations are in a physiological range for many clinically interesting blood serum proteins. The results of this type of analysis for each antigen tested are presented in the table below. Antibodies were classified according to the presence of accurate quantitation over the entire range for all of the low background trial and at least part of the higher background trials (++). They were classified as (+) if they showed accurate quantitation for most of the low background trial. Many of the antibodies showed either no signal or non-specific signal.

In a second mode of detection, antigens were spotted onto the array to detect labeled antibodies. Figure 7 presents an example of specific detection of antibodies in four unique mixes. A combinatorial labeling scheme was employed that enabled identification of specific antigen/antibody binding. An analysis similar to that described above was carried out to classify the binding specificity of antigens on the microarray. The results of that analysis are presented in the table below along with the antibody array results. According to this analysis, the protein array works at least as well or better using spotted antigens as compared to spotted antibodies.

Antibody/antigen	Antibody array ++	+	-	Part. conc. limit	Antigen array ++	+	-
Anti-AIM-1	x			1.00E-06	x		
Anti-HCG	x				x		
Anti-MAP4	x				x		
Anti-Per2	x				x		
Anti-Flag (new)	x						x
Anti-Alpha HCG	x			4.00E-08		x	
Anti-Fc. IgG	x			1.00E-07			x
Anti-Flag (old)	x						
Anti-Human IgG	x						
Anti-Mint2	x					x	
Anti-Sin	x						x
Anti-SOD	x					x	
Anti-ABR		x		6.00E-05	x		
Anti-AKAP-KL		x			x		
Anti-Dematin		x		1.00E-04	x		
Anti-Dlg		x			x		
Anti-DSIF		x			x		
Anti-FIN13		x			x		
Anti-HDAC3		x			x		
Anti-HIF-1alpha		x			x		
Anti-ICH-IL		x			x		
Anti-IGF2R		x			x		
Anti-Kanadaptin		x			x		
Anti-La		x			x		
Anti-LAIR-1		x			x		
Anti-LAP2		x			x		
Anti-MEKK3		x			x		
Anti-Mint1		x			x		
Anti-MST3		x			x		
Anti-p19 Skp1		x			x		
Anti-p38 gamma		x			x		
Anti-Rab4		x			x		
Anti-TEF-1		x			x		
Anti-ZO-1		x			x		

Anti-Tropomyosin		x						
Anti-Alkaline phosphatase		x					x	
Anti-cTnI		x		4.00E-04			x	
Anti-DFF45		x					x	
Anti-Fibronectin		x					x	
Anti-GOK		x						x
Anti-GS15		x					x	
Anti-Insulin		x					x	
Anti-LAT		x					x	
Anti-MAD-3		x						
Anti-mGluR1		x					x	
Anti-MST1		x					x	
Anti-Myoglobin (ResGen)		x					x	
Anti-Myoglobin (Sigma)		x						
Anti-Neuroglycan C		x					x	
Anti-PSA 2F5		x					x	
Anti-PSA F5		x						
Anti-Rad50		x					x	
Anti-RBC		x						x
Anti-Rim		x					x	
Anti-ROCK-1		x						x
Anti-SRPK1		x						x
Anti-VLA-3alpha		x						x
Anti-Adaptin alpha			x		x			
Anti-Bax			x		x			
Anti-Calretinin			x		x			
Anti-c-Cbl			x		x			
Anti-Clathrin H			x		x			
Anti-DEK			x		x			
Anti-DGK0			x		x			
Anti-Efp			x		x			
Anti-erg2			x		x			
Anti-hHR23B			x		x			
Anti-Kalinin B1			x		x			
Anti-PUNTS			x		x			

Anti-RNCAM			x		x	
Anti-SRP54			x		x	
Anti-TFII-I			x		x	
Anti-TIF2			x		x	
Anti-TSP-1			x		x	
Anti-VHR			x		x	
Anti-AKAP149			x			x
Anti-alpha acid glycoprotein (AGP)			x			x
Anti-Annexin II			x			x
Anti-ARNT1			x			x
Anti-Brm			x			x
Anti-Calmodulin			x			x
Anti-Calnexin			x			x
Anti-CaM K IV			x			x
Anti-CAS			x			
Anti-CLA-1			x			x
Anti-CRP			x			x
Anti-Cyclin A			x			
Anti-DNA pol delta			x			x
Anti-eIF-5			x			x
Anti-ERp72			x			x
Anti-ESA			x			x
Anti-G3VP			x			x
Anti-Gelsolin			x			x
Anti-Hsp70			x			x
Anti-Hsp90			x			x
Anti-IAK-1			x			x
Anti-IQGAP1			x			x
Anti-KAP3A			x			x
Anti-Ki-67			x			x
Anti-LRP			x			x
Anti-MEK5			x			x
Anti-Neurabin			x			x
Anti-Numb			x			x
Anti-PARP			x			x

Anti-Pax-5			x				x
Anti-PDI			x				x
Anti-PI3-K p170			x			x	
Anti-rSec8			x			x	
Anti-SIRPalpha1			x				x
Anti-Smad4			x				x
Anti-TAF-172			x				x
Anti-TIAR			x			x	
Anti-Transportin			x				x
Anti-Utrophin			x				x

it is apparent from the above experimental data and descriptions that the subject methods provide a useful method for constructing a microarray comprising immobilized polypeptides. The polypeptides retain the binding specificity, and are useful in the detection and quantitation of ligands that bind to polypeptides, including proteins and fragments thereof, peptides, nucleic acids, factors and co-factors, and the like.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

WHAT IS CLAIMED IS:

1. A method of simultaneously detecting the presenc of multiple protein-binding ligands in a sample, the method comprising:

contacting said sample with a microarray of polypeptides, wherein said microarray comprises 100 or more discrete regions of distinct polypeptide strands per cm^2 of solid planar support;

washing said support free of unbound sample; and

detecting the presence of bound ligands.

2. The method of Claim 1, wherein the ligands present in said sample are labeled with a detectable label.

3. The method of Claim 2, wherein said detectable label is a fluorochrome.

4. The method of Claim 2, further comprising contacting said microarray with a second sample comprising ligands labeled with a second detectable label.

5. The method of Claim 4, wherein said second detectable label is a fluorochrome.

6. The method according to Claim 1, wherein said sample is a clinical sample of a physiological fluid.

7. The method according to Claim 6, wherein said physiological fluid is blood or a derivative thereof.

8. The method of Claim 1, wherein said sample is a cell culture supernatant.

9. The method of Claim 1, wherein said sample is a cell lysate.

10. The method according to Claim 1, wherein said polypeptides are antibodies.

11. The method of Claim 1, wherein said polypeptides are antigens.

12. The method of Claim 1, wherein said polypeptides are at least 50 amino acids in length.

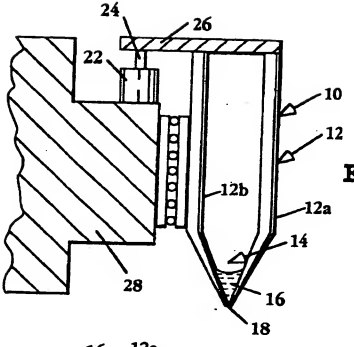


Fig. 1

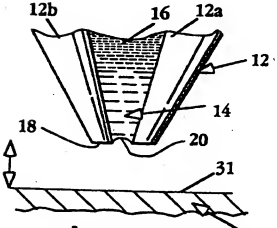


Fig. 2A

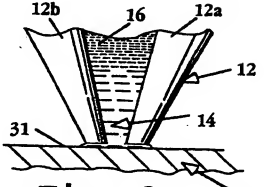


Fig. 2B

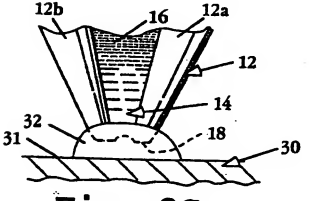


Fig. 2C

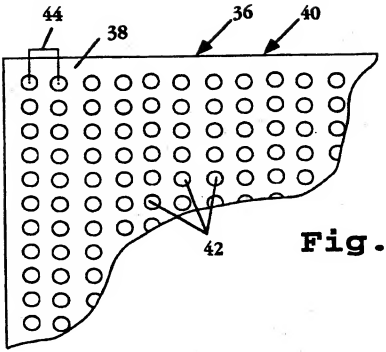

44
38
36
40
42

Fig. 3

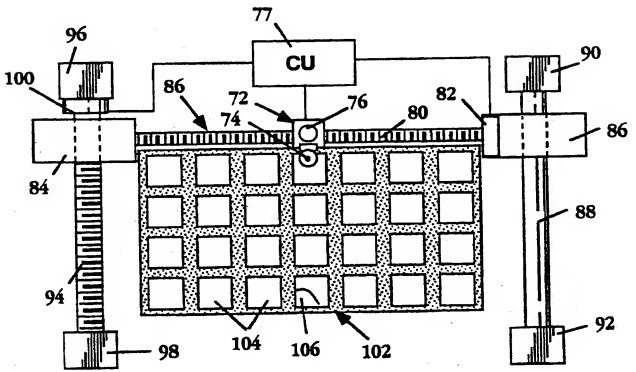

77
CU
96
100
86
72
74
76
80
82
90
86
84
88
94
92
98
104
106
102

Fig. 4

FIGURE 5

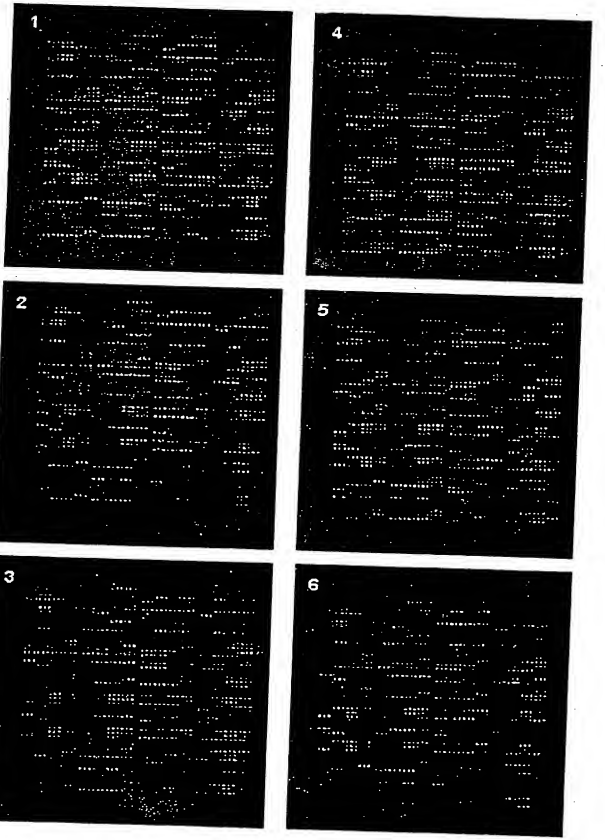


FIGURE 6

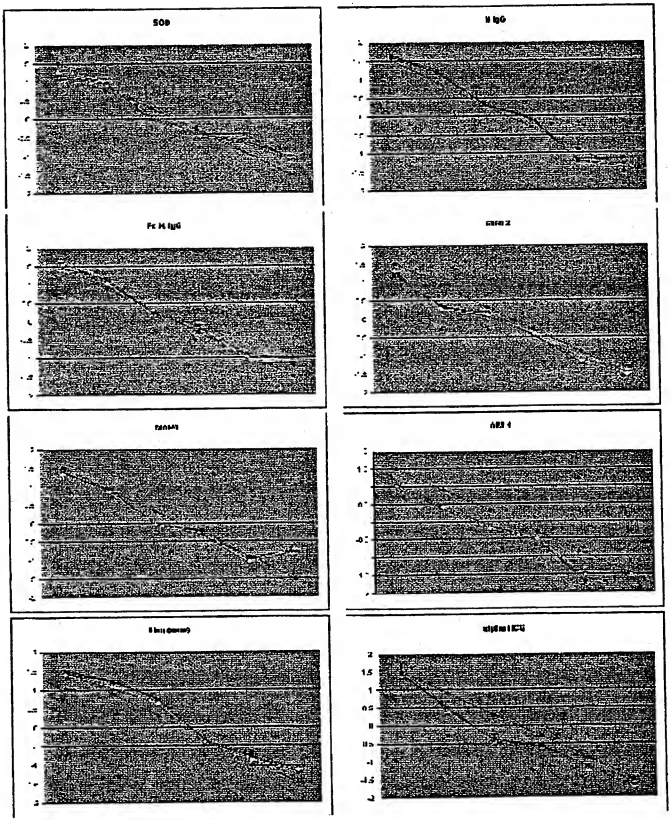
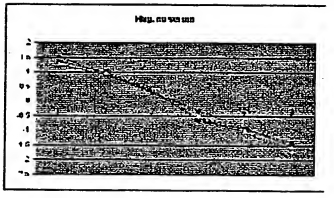
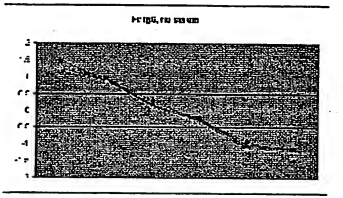


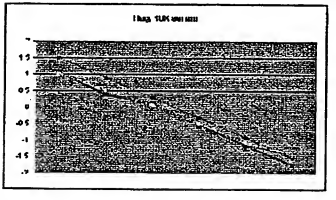
FIGURE 7

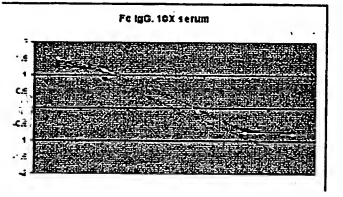
Fc h. IgG

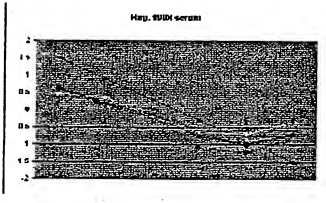
Flag











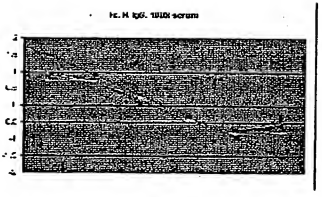
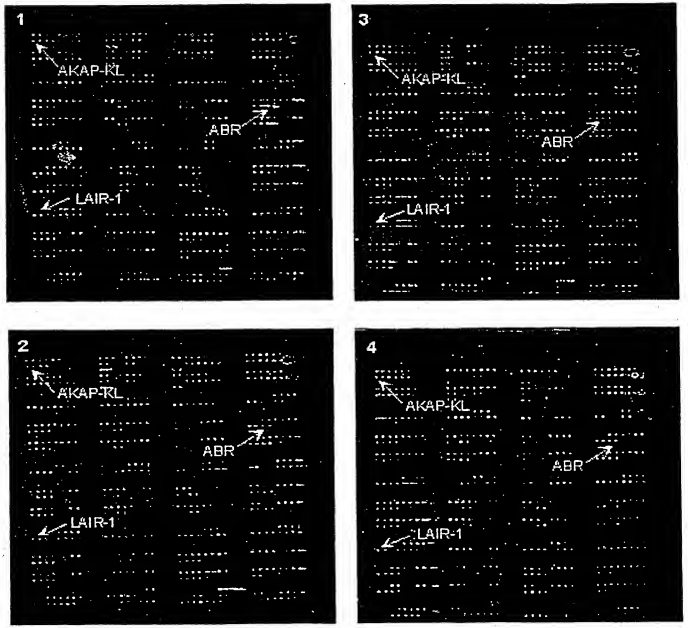


FIGURE 8



	mix 1	mix 2	mix 3	mix 4
AKAP-KL	1	2	3	2
LAIR-1	1	2	2	3
ABR	3	1	2	3

0 = blank
1 = green
2 = red
3 = yellow

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
26 October 2000 (26.10.2000)

PCT

(10) International Publication Number
WO 00/63701 A3

(51) International Patent Classification⁷: G01N 33/68, B01J 19/00

(21) International Application Number: PCT/US00/10171

(22) International Filing Date: 14 April 2000 (14.04.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/129,449 15 April 1999 (15.04.1999) US

(71) Applicant *(for all designated States except US)*: **THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY** [US/US]; 900 Welch Road, Suite 350, Palo Alto, CA 94304 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **BROWN, Patrick** [US/US]; 76 Peter Coutts Circle, Stanford, CA 94305 (US). **HAAB, Brian** [US/US]; 1922 Grant #1, Berkeley, CA 94703 (US).

(74) Agent: **SHERWOOD, Pamela, J.**; Bozicevic, Field & Francis LLP, 200 Middlefield Road, Suite 200, Menlo Park, CA 94025 (US).

(81) Designated States *(national)*: CA, JP, US.

(84) Designated States *(regional)*: European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

Published:
— *With international search report.*

(88) Date of publication of the international search report:
8 March 2001

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 00/63701 A3

(54) Title: MICROARRAYS OF POLYPEPTIDES

(57) Abstract: Microarrays of polypeptides on a solid support are provided. The microarray compositions find use in the multiplexed detection and quantitation of ligands; *e.g.* antigens or antibodies, in a miniaturized format. The substrate is used for detecting binding of ligands to a plurality of polypeptides for screening and diagnostic purposes.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 00/10171

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 G01N33/68 B01J19/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 G01N B01J

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 5 807 522 A (PATRICK O. BROWN & TIDHAR DARI SHALON) 15 September 1998 (1998-09-15) column 3, line 23 - line 35 column 4, line 17 - line 23 column 6, line 32 - line 37 column 14, line 19 - line 34 column 15, line 5 - line 58	1-12
X	WO 97 42507 A (ISIS INNOVATION LIMITED) 13 November 1997 (1997-11-13) abstract page 3, line 15 -page 4, line 16 page 7, line 18 - line 25 page 9, line 14 -page 10, line 3 page 4, line 14 - line 26	1-12

-/--

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
11 October 2000	18/10/2000

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Stevnsborg, N

1

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	US 5 324 633 A (STEPHEN P.A. FODOR & LAURA T. MAZZOLA) 28 June 1994 (1994-06-28) abstract column 3, line 47 - line 60 column 5, line 21 - line 38 column 6, line 3 - line 61 column 10, line 21 -column 11, line 17	1-12
X	JEFFREY W. JACOBS & STEPHEN P.A. FODOR: "COMBINATORIAL CHEMISTRY - APPLICATIONS OF LIGHT DIRECTED CHEMICAL SYNTHESIS" TIBTECH, vol. 12, no. 1, 1994, pages 19-26, XP000652268 CAMBRIDGE, UK the whole document	1-12
X	STEPHEN P.A. FODOR ET AL.: "LIGHT-DIRECTED, SPATIALLY ADDRESSABLE PARALLEL CHEMICAL SYNTHESIS" SCIENCE, vol. 251, no. 4995, 15 February 1991 (1991-02-15), pages 767-773, XP000486899 US ISSN: 0036-8075 cited in the application the whole document	1-12
X	S. M. RUBER ET AL.: "LIGHT-DIRECTED COMBINATORIAL PEPTIDE SYNTHESIS" 1992 , PROCEEDINGS OF THE 12TH AMERICAN PEPTIDE SYMPOSIUM, 16-21 JUNE 1991, CAMBRIDGE, MA, USA , LEIDEN, NL XP000371924 185690 page 489 -page 491	1-12
X	RONALD FRANK : "SPOT-SYNTHESIS: AN EASY TECHNIQUE FOR THE POSITIONALLY ADDRESSABLE, PARALLEL CHEMICAL SYNTHESIS ON A MEMBRANE SUPPORT" TETRAHEDRON, vol. 48, no. 42, 16 October 1992 (1992-10-16), pages 9217-9232, XP000353580 UK ISSN: 0040-4020 page 9217 -page 9232	1-12

-/—

1

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	CHRISTOPHER P. HOLMES ET AL.: "THE USE OF LIGHT-DIRECTED COMBINATORIAL PEPTIDE SYNTHESIS IN EPITOPE MAPPING" BIOPOLYMERS (PEPTIDE SCIENCE), vol. 37, no. 3, 1995, pages 199-211, XP000654595 NEW YORK, US ISSN: 0006-3525 page 199 -page 211 _____	1-12

1

INTERNATIONAL SEARCH REPORT

Information on patent family members

Int ional Application No
PCT/US 00/10171

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
US 5807522 A	15-09-1998	AT 180570 T	15-06-1999
		AU 709276 B	26-08-1999
		AU 2862995 A	15-01-1996
		CA 2192095 A	28-12-1995
		DE 69509925 D	01-07-1999
		DE 69509925 T	09-12-1999
		EP 0804731 A	05-11-1997
		EP 0913485 A	06-05-1999
		ES 2134481 T	01-10-1999
		GR 3030430 T	30-09-1999
		JP 10503841 T	07-04-1998
		US 6110426 A	29-08-2000
		WO 9535505 A	28-12-1995
WO 9742507 A	13-11-1997	NONE	
US 5324633 A	28-06-1994	NONE	

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

CORRECTED VERSION

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
26 October 2000 (26.10.2000)

PCT

(10) International Publication Number
WO 00/63701 A3

(51) International Patent Classification[7]: G01N 33/68. B01J 19/00

(21) International Application Number: PCT/US00/10171

(22) International Filing Date: 14 April 2000 (14.04.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/129,449 15 April 1999 (15.04.1999) US

(71) Applicant *(for all designated States except US)*: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY [US/US]; 900 Welch Road, Suite 350, Palo Alto, CA 94304 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: BROWN, Patrick [US/US]; 76 Peter Coutts Circle, Stanford, CA 94305 (US). HAAB, Brian [US/US]; 1922 Grant #1, Berkeley, CA 94703 (US).

(74) Agent: SHERWOOD, Pamela, J.; Bozicevic, Field & Francis LLP, 200 Middlefield Road, Suite 200, Menlo Park, CA 94025 (US).

(81) Designated States *(national)*: CA, JP, US.

(84) Designated States *(regional)*: European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

Published:
— *with international search report*

(88) Date of publication of the international search report:
8 March 2001

(48) Date of publication of this corrected version:
27 June 2002

(15) Information about Correction:
see PCT Gazette No. 26/2002 of 27 June 2002, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 00/63701 A3

(54) Title: MICROARRAYS OF POLYPEPTIDES

(57) Abstract: Microarrays of polypeptides on a solid support are provided. The microarray compositions find use in the multiplexed detection and quantitation of ligands, *e.g.* antigens or antibodies, in a miniaturized format. The substrate is used for detecting binding of ligands to a plurality of polypeptides for screening and diagnostic purposes.

MICROARRAYS OF POLYPEPTIDES

FIELD OF THE INVENTION

This invention relates to methods and apparatus for fabricating microarrays of biological samples, and the uses thereof.

BACKGROUND OF THE INVENTION

Life and development of all organisms are determined by molecular interactions, *e.g.* between DNA and proteins, proteins and proteins, or proteins and small molecules. Among these, protein-protein interactions play an especially important role, for example with the interactions between antibodies and antigens, receptors and peptide- or protein-hormones, enzymes and substrates or inhibitors. Many of the best-selling drugs either act by targeting proteins or are proteins. In addition, many molecular markers of disease, which are the basis of diagnostics, are proteins.

The development of techniques and reagents for high throughput protein analysis has been of great interest. In particular, the increasing knowledge of DNA sequence in organisms of interest has spurred interest in protein expression analysis. There is now a rapidly growing awareness of just how important proteomics is to understand and organize the human genome. Information about the complement of proteins present in a cell is a key to accelerate the discovery of medically important proteins and the genes from which they derive.

Genomics establishes the relationship between gene activity and particular diseases. However most disease processes are manifested not at the level of genes, but at the protein level. There is often a poor correlation between the level of activity of different genes and the relative abundance of the corresponding proteins. Also a protein and its post-translational modifications are not directly encoded for by the same gene, therefore the complete structure of individual proteins cannot be determined by reference to the gene alone.

Assays directed towards protein binding can be used for the quantitation of protein expression; the determination of specific interactions; to determine the presence of ligands for a protein, and the like. Methods of quantitating proteins in a sample by determining binding to a cognate antibody are known in the art.

For example, solid-phase radioimmunoassay (RIA) of antigens or antibodies in a serum sample are well known. Catt *et al.* have reported such techniques on the surface of plastic tubes (U.S. Pat. No. 3,646,346) and plastic discs (J. Lab. & Clin. Med., 70: 820 (1967). In such techniques, an excess of specific antibody is first adsorbed to a support

surface. Then, the sample to be assayed is immunologically reacted with such surface in a sandwich or competitive binding technique. In the competitive binding technique, illustrated in U.S. Pat. No. 3,555,143, the concentration of antigen to be determined and a known quantity of radioactively tagged antigen are immunologically reacted with the antibody-adsorbed surface. The labeled antigen bound to the antibody on the surface is then quantitated to determine indirectly the total quantity of antigen in the original sample. In the sandwich technique, serum containing an unknown concentration of antigen is immunologically reacted with the antibody-containing surface. Then in a following step, the bound antigen is incubated with labeled antibody and the amount of immunologically bound, labeled antibody is subsequently measured.

The development of high-throughput, parallel systems for protein analysis are of great interest, particularly where the analysis can use small amounts of material for analysis. Preferably such systems provide for the use of complex molecules with high binding affinity for their ligands, such as antibodies, protein receptors, and the like.

Literature:

Publications of interest include: Abouzied, et al., Journal of AOAC International 77(2):495-500 (1994). Bohlander, et al., Genomics 13:1322-1324 (1992). Drmanac, et al., Science 260:1649-1652 (1993). Fodor, et al., Science 251:767-773 (1991). Khrapko, et al., DNA Sequence 1:375-388 (1991). Kuriyama, et al., An Isfet Biosensor, Applied Biosensors (Donald Wise, Ed.), Butterworths, pp. 93-114 (1989). Lehrach, *et al.*, Hybridization Fingerprinting in Genome Mapping And Sequencing, Genome Analysis, Vol 1 (Davies and Tilgham, Eds.), Cold Spring Harbor Press, pp. 39-81 (1990). Maniatis, et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press (1989). Nelson, et al., Nature Genetics 4:11-18 (1993). Pirrung, et al., U.S. Pat. No. 5,143,854 (1992). Riles, et al., Genetics 134:81-150 (1993). Schena, M. et al., Proc. Nat. Acad. Sci. USA 89:3894-3898 (1992). Southern, et al., Genomics 13:1008-1017 (1992).

SUMMARY OF THE INVENTION

Methods are provided for forming a microarray of analyte-assay regions on a solid support, where each region in the array has a known amount of a selected, analyte-specific reagent. The method involves first loading a solution of a selected analyte-specific reagent in a reagent-dispensing device having an elongate capillary channel (i) formed by spaced-apart, coextensive elongate members, (ii) adapted to hold a quantity of the reagent solution and (iii) having a tip region at which aqueous solution in the channel forms a meniscus. Th channel is preferably formed by a pair of spaced-apart tapered elements. The microarray

compositions find use in the multiplexed detection and quantitation of ligands, *e.g.* antigens or antibodies, in a miniaturized format.

In another aspect, the invention includes a substrate with a surface having a microarray of at least 10^3 distinct polynucleotide or polypeptide biopolymers in a surface area of less than about 1 cm^2. Each distinct biopolymer is disposed at a separate, defined position in said array, has a length of at least 50 subunits, and is present in a defined amount between about 0.1 femtomoles and 100 nanomoles.

The substrate may be used for detecting binding of ligands to a plurality of different-sequence, immobilized biopolymers. The substrate includes, in one aspect, a glass support, a coating of a polycationic polymer, such as polylysine, on said surface of the support, and an array of distinct biopolymers electrostatically bound non-covalently to said coating, where each distinct biopolymer is disposed at a separate, defined position in a surface array.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a side view of a reagent-dispensing device having a open-capillary dispensing head constructed for use in one embodiment of the invention;

FIGS. 2A-2C illustrate steps in the delivery of a fixed-volume bead on a hydrophobic surface employing the dispensing head from FIG. 1, in accordance with one embodiment of the method of the invention;

FIG. 3 shows a portion of a two-dimensional array of analyte-assay regions constructed according to the method of the invention;

FIG. 4 is a planar view showing components of an automated apparatus for forming arrays in accordance with the invention.

FIG. 5 shows the concentration profiles in a microarray of 110 antigens.

FIG. 6 shows the detection of protein as a ratio of the signal from two fluorochromes, against the dilution of the protein sample.

FIG. 7 shows graphs of the protein quantitation after dilution into serum.

FIG. 8 depicts the combinatorial detection of multiple antibodies.

DETAILED DESCRIPTION OF THE INVENTION

Methods and compositions are provided for forming a microarray of polypeptide regions on a solid support, where each region in the array has a known amount of a selected polypeptide. A robotic printer is used to deposit microdrops of protein solutions onto a derivatized planar surface substrate, where the derivatized surface binds the polypeptide, *e.g.* poly-lysine, and the like. The substrate with a surface having a microarray is spott d at a high density, usually of at least 10^3 distinct polypeptide in a surface area of less than about

1 cm^2. Each distinct polypeptide is present in a defined amount between about 0.1 femtomoles and 100 nanomoles. Any polypeptide can be used, although generally the polypeptide will be at least about 50 amino acids in length.

The microarrays are widely used in quantitative and analytical methods for the detection and quantitation of proteins, or compounds that interact with proteins, such as polynucleotides, hormones, vitamins and other co-factors, *etc.* Typically a sample comprising ligands that are suspected of binding to a polypeptide immobilized on the microarray are added to the microarray under conditions that allow specific binding between the polypeptide and the ligand. The unbound sample is washed from the microarray, and the bound ligand is detected by any suitable method, *e.g.* through the use of detectable labels present on the ligand, or provided in a second, detecting step. Sample consumption is much lower than traditional immunoassays due to the highly parallel and miniaturized format of the present invention. The quantitative measurement of many components in parallel allows diagnosis and recognition of physiological and phenotypic characteristics of a sample to be based on a multidimensional pattern of expression, rather than simply a few parameters.

In one embodiment of the invention, comparative fluorescence is used to monitor the presence of bound ligands to the microarray. The use of comparative fluorescence measurements allows greater precision across a wide range of ligand concentrations and binding affinities, as compared to methods that measure the absolute amount of bound ligand.

In one embodiment of the invention, the biopolymers are polypeptides, *e.g.* antigens, antibodies, receptors, *etc.*, that have functional binding properties imparted by the three-dimensional structure of the polypeptide, which structure is frequently dependent on contacts made between non-contiguous amino acid residues, such as disulphide bonds between cysteine residues, hydrophobic pockets, and the like. Such binding properties include the specific binding between a protein receptor and one or more of its naturally occurring ligands, for example cytokines and cytokine receptors, hormones and hormone receptors, chemokines and chemokine receptors, *etc.*, including a range of protein and polypeptide molecules that provide for specific interactions within a biological system. DNA binding proteins, *e.g.* nuclear hormone receptors; transcription factors, *etc.* may be provided on a microarray, where the proteins retain the ability to specifically define their cognate DNA motif. Microarrays that maintain binding properties of antigen specific immunological receptors are of particular interest, which receptors include antibodies, T cell antigen receptors, and major histocompatibility complex proteins.

These and other objects and features of the invention will become more fully apparent when the following detailed description of the invention is read in conjunction with the accompanying figures.

Definitions

Unless indicated otherwise, the terms defined below have the following meanings:

"*Ligand*" refers to one member of a ligand/anti-ligand binding pair. The ligand may be, for example, one of the nucleic acid strands in a complementary, hybridized nucleic acid duplex binding pair; an effector molecule in an effector/receptor binding pair; or an antigen in an antigen/antibody or antigen/antibody fragment binding pair.

"*Anti-ligand*" refers to the opposite member of a ligand/anti-ligand binding pair. The anti-ligand may be the other of the nucleic acid strands in a complementary, hybridized nucleic acid duplex binding pair; the receptor molecule in an effector/receptor binding pair; or an antibody or antibody fragment molecule in antigen/antibody or antigen/antibody fragment binding pair, respectively.

"*Analyte*" or "*analyte molecule*" refers to a molecule, typically a macromolecule, such as a polynucleotide or polypeptide, whose presence, amount, and/or identity are to be determined. The analyte is one member of a ligand/anti-ligand pair.

"*Analyte-specific assay reagent*" refers to a molecule effective to bind specifically to an analyte molecule. The reagent is the opposite member of a ligand/anti-ligand binding pair.

An "*array of regions on a solid support*" is a linear or two-dimensional array of preferably discrete regions, each having a finite area, formed on the surface of a solid support.

A "*microarray*" is an array of regions having a density of discrete regions of at least about 100/cm^2, and preferably at least about 1000/cm^2. The regions in a microarray have typical dimensions, *e.g.*, diameters, in the range of between about 10-250 μm, and are separated from other regions in the array by about the same distance.

A support surface is "*hydrophobic*" if a aqueous-medium droplet applied to the surface does not spread out substantially beyond the area size of the applied droplet. That is, the surface acts to prevent spreading of the droplet applied to the surface by hydrophobic interaction with the droplet.

A "*meniscus*" means a concave or convex surface that forms on the bottom of a liquid in a channel as a result of the surface tension of the liquid.

"*Distinct biopolymers*", as applied to the biopolymers forming a microarray, means an array member which is distinct from other array members on the basis of a different biopolymer sequence, and/or different concentrations of the sam or distinct biopolymers,

and/or different mixtures of distinct or different-concentration biopolymers. Thus an array of "distinct polynucleotides" means an array containing, as its members, (i) distinct polynucleotides, which may have a defined amount in each member, (ii) different, graded concentrations of given-sequence polynucleotides, and/or (iii) different-composition mixtur s of two or more distinct polynucleotides.

"*Cell type*" means a cell from a given source, e.g., a tissue, or organ, or a cell in a given state of differentiation, or a cell associated with a given pathology or genetic makeup.

Method of Microarray Formation

This section describes a method of forming a microarray of analyte-assay regions on a solid support or substrate, where each region in the array has a known amount of a selected, analyte-specific reagent.

FIG. 1 illustrates, in a partially schematic view, a reagent-dispensing device 10 useful in practicing the method. The device generally includes a reagent dispenser 12 having an elongate open capillary channel 14 adapted to hold a quantity of the reagent solution, such as indicated at 16, as will be described below. The capillary channel is formed by a pair of spaced-apart, coextensive, elongate members 12a, 12b which are tapered toward one another and converge at a tip or tip region 18 at the lower end of the channel. More generally, the open channel is formed by at least two elongate, spaced-apart members adapted to hold a quantity of reagent solutions and having a tip region at which aqueous solution in the channel forms a meniscus, such as the concave meniscus illustrated at 20 in FIG. 2A. The advantages of the open channel construction of the dispenser are discussed below.

With continued reference to FIG. 1, the dispenser device also includes structure for moving the dispenser rapidly toward and away from a support surface, for effecting deposition of a known amount of solution in the dispenser on a support, as will be described below with reference to FIGS. 2A-2C. In the embodiment shown, this structure includes a solenoid 22 which is activatable to draw a solenoid piston 24 rapidly downwardly, then release the piston, e.g., under spring bias, to a normal, raised position, as shown. The dispenser is carried on the piston by a connecting member 26, as shown. The just-described moving structure is also referred to herein as dispensing means for moving the dispenser into engagement with a solid support, for dispensing a known volume of fluid on the support.

The dispensing device just described is carried on an arm 28 that may be moved either linearly or in an x-y plane to position the dispenser at a selected deposition position, as will be described.

FIGS. 2A-2C illustrate the method of depositing a known amount of reagent solution in the just-described dispenser on the surface of a solid support, such as the support indicated at 30. The support is a polymer, glass, or other solid-material support having a surface indicated at 31.

In one general embodiment, the surface is a relatively hydrophilic, i.e., wettable surface, such as a surface having native, bound or covalently attached charged groups. One such surface described below is a glass surface having an absorbed layer of a polycationic polymer, such as poly-l-lysine.

In another embodiment, the surface has or is formed to have a relatively hydrophobic character, i.e., one that causes aqueous medium deposited on the surface to bead. A variety of known hydrophobic polymers, such as polystyrene, polypropylene, or polyethylene have desired hydrophobic properties, as do glass and a variety of lubricant or other hydrophobic films that may be applied to the support surface.

Initially, the dispenser is loaded with a selected analyte-specific reagent solution, such as by dipping the dispenser tip, after washing, into a solution of the reagent, and allowing filling by capillary flow into the dispenser channel. The dispenser is now moved to a selected position with respect to a support surface, placing the dispenser tip directly above the support-surface position at which the reagent is to be deposited. This movement takes place with the dispenser tip in its raised position, as seen in FIG. 2A, where the tip is typically at least several 1-5 mm above the surface of the substrate.

With the dispenser so positioned, solenoid 22 is now activated to cause the dispenser tip to move rapidly toward and away from the substrate surface, making momentary contact with the surface, in effect, tapping the tip of the dispenser against the support surface. The tapping movement of the tip against the surface acts to break the liquid meniscus in the tip channel, bringing the liquid in the tip into contact with the support surface. This, in turn, produces a flowing of the liquid into the capillary space between the tip and the surface, acting to draw liquid out of the dispenser channel, as seen in FIG. 2B.

FIG. 2C shows flow of fluid from the tip onto the support surface, which in this case is a hydrophobic surface. The figure illustrates that liquid continues to flow from the dispenser onto the support surface until it forms a liquid bead 32. At a given bead size, i.e., volume, the tendency of liquid to flow onto the surface will be balanced by the hydrophobic surface interaction of the bead with the support surface, which acts to limit the total bead area on the surface, and by the surface tension of the droplet, which tends toward a given bead curvature. At this point, a given bead volume will have formed, and continued contact of the dispenser tip with the bead, as the dispenser tip is being withdrawn, will have little or no effect on bead volume.

For liquid-dispensing on a more hydrophilic surface, the liquid will have less of a tendency to bead, and the dispensed volume will be more sensitive to the total dwell time of the dispenser tip in the imm diate vicinity of the support surface, e.g., the positions illustrated in FIGS. 2B and 2C.

The desired deposition volume, i.e., bead volume, formed by this method is preferably in the range 2 pl (picoliters) to 2 nl (nanoliters), although volumes as high as 100 nl or more may be dispensed. It will be appreciated that the selected dispensed volume will depend on (i) the "footprint" of the dispenser tip, i.e., the size of the area spanned by the tip, (ii) the hydrophobicity of the support surface, and (iii) the time of contact with and rate of withdrawal of the tip from the support surface. In addition, bead size may be reduced by increasing the viscosity of the medium, effectively reducing the flow time of liquid from th dispenser onto the support surface. The drop size may be further constrained by depositing the drop in a hydrophilic region surrounded by a hydrophobic grid pattern on the support surface.

In a typical embodiment, the dispenser tip is tapped rapidly against the support surface, with a total residence time in contact with the support of less than about 1 msec, and a rate of upward travel from the surface of about 10 cm/sec.

Assuming that the bead that forms on contact with the surface is a hemispherical bead, with a diameter approximately equal to the width of the dispenser tip, as shown in FIG. 2C, the volume of the bead formed in relation to dispenser tip width (d) is given in Table 1 below. As seen, the volume of the bead ranges between 2 pl to 2 nl as the width size is increased from about 20 to 200 μm.

TABLE 1

d	Volume (nl)
20 μm	2×10^{-3}
50 μm	3.1×10^{-2}
100 μm	2.5×10^{-1}
200 μ	2

At a given tip size, bead volume can be reduced in a controlled fashion by increasing surface hydrophobicity, reducing time of contact of the tip with the surface, increasing rate of movement of the tip away from the surface, and/or increasing the viscosity of the medium. Once these parameters are fixed, a selected deposition volume in the desired pl to nl range can be achieved in a repeatable fashion.

After depositing a bead at one selected location on a support, the tip is typically moved to a corresponding position on a second support, a droplet is deposited at that position, and this process is repeated until a liquid droplet of the reagent has been deposited at a selected position on each of a plurality of supports.

The tip is then washed to remove the reagent liquid, filled with another reagent liquid and this reagent is now deposited at each another array position on each of the supports. In one embodiment, the tip is washed and refilled by the steps of (i) dipping the capillary channel of the device in a wash solution, (ii) removing wash solution drawn into the capillary channel, and (iii) dipping the capillary channel into the new reagent solution.

From the foregoing, it will be appreciated that the tweezers-like, open-capillary dispenser tip provides the advantages that (i) the open channel of the tip facilitates rapid, efficient washing and drying before reloading the tip with a new reagent, (ii) passive capillary action can load the sample directly from a standard microwell plate while retaining sufficient sample in the open capillary reservoir for the printing of numerous arrays, (iii) open capillaries are less prone to clogging than closed capillaries, and (iv) open capillaries do not require a perfectly faced bottom surface for fluid delivery.

A portion of a microarray 36 formed on the surface 38 of a solid support 40 in accordance with the method just described is shown in FIG. 3. The array is formed of a plurality of analyte-specific reagent regions, such as regions 42, where each region may include a different analyte-specific reagent. As indicated above, the diameter of each region is preferably between about 20-200 μm. The spacing between each region and its closest (non-diagonal) neighbor, measured from center-to-center (indicated at 44), is preferably in the range of about 20-400 μm. Thus, for example, an array having a center-to-center spacing of about 250 μm contains about 40 regions/cm or 1,600 regions/cm^2. After formation of the array, the support is treated to evaporate the liquid of the droplet forming each region, to leave a desired array of dried, relatively flat regions. This drying may be done by heating or under vacuum.

In some cases, it is desired to first rehydrate the droplets containing the analyte reagents to allow for more time for adsorption to the solid support. It is also possible to spot out the analyte reagents in a humid environment so that droplets do not dry until the arraying operation is complete.

Automated Apparatus for Forming Arrays

In another aspect, the invention includes an automated apparatus for forming an array of analyte-assay regions on a solid support, where each region in the array has a known amount of a selected, analyte-specific reagent.

The apparatus is shown in planar, and partially schematic view in FIG. 4. A dispenser device 72 in the apparatus has the basic construction described above with respect to FIG. 1, and includes a dispenser 74 having an open-capillary channel terminating at a tip, substantially as shown in FIGS. 1 and 2A-2C.

The dispenser is mounted in the device for movement toward and away from a dispensing position at which the tip of the dispenser taps a support surface, to dispense a selected volume of reagent solution, as described above. This movement is effected by a solenoid 76 as described above. Solenoid 76 is under the control of a control unit 77 whos operation will be described below. The solenoid is also referred to herein as dispensing means for moving the device into tapping engagement with a support, when the device is positioned at a defined array position with respect to that support.

The dispenser device is carried on an arm 74 which is threadedly mounted on a worm screw 80 driven (rotated) in a desired direction by a stepper motor 82 also under the control of unit 77. At its left end in the figure screw 80 is carried in a sleeve 84 for rotation about the screw axis. At its other end, the screw is mounted to the drive shaft of the stepper motor, which in turn is carried on a sleeve 86. The dispenser device, worm screw, the two sleeves mounting the worm screw, and the stepper motor used in moving the device in the "x" (horizontal) direction in the figure form what is referred to here collectively as a displacement assembly 86.

The displacement assembly is constructed to produce precise, micro-range movement in the direction of the screw, i.e., along an x axis in the figure. In one mode, the assembly functions to move the dispenser in x-axis increments having a selected distance in the range 5-25 μm. In another mode, the dispenser unit may be moved in precise x-axis increments of several microns or more, for positioning the dispenser at associated positions on adjacent supports, as will be described below.

The displacement assembly, in turn, is mounted for movement in the "y" (vertical) axis of the figure, for positioning the dispenser at a selected y axis position. The structure mounting the assembly includes a fixed rod 88 mounted rigidly between a pair of frame bars 90, 92, and a worm screw 94 mounted for rotation between a pair of frame bars 96, 98. The worm screw is driven (rotated) by a stepper motor 100 which operates under the control of unit 77. The motor is mounted on bar 96, as shown.

The structure just described, including worm screw 94 and motor 100, is constructed to produce precise, micro-range movement in the direction of the screw, i.e., along a y axis in the figure. As above, the structure functions in one mode to move the dispenser in y-axis increments having a selected distance in the range 5-250 μm, and in a second mode, to

move the dispenser in precise y-axis increments of several microns (μm) or more, for positioning the dispenser at associated positions on adjacent supports.

The displacement assembly and structure for moving this assembly in the y axis are referred to herein collectively as positioning means for positioning the dispensing device at a selected array position with respect to a support.

A holder 102 in the apparatus functions to hold a plurality of supports, such as supports 104 on which the microarrays of reagent regions are to be formed by the apparatus. The holder provides a number of recessed slots, such as slot 106, which receive the supports, and position them at precise selected positions with respect to the frame bars on which the dispenser moving means is mounted.

As noted above, the control unit in the device functions to actuate the two stepper motors and dispenser solenoid in a sequence designed for automated operation of the apparatus in forming a selected microarray of reagent regions on each of a plurality of supports.

The control unit is constructed, according to conventional microprocessor control principles, to provide appropriate signals to each of the solenoid and each of the stepper motors, in a given timed sequence and for appropriate signaling time. The construction of the unit, and the settings that are selected by the user to achieve a desired array pattern, will be understood from the following description of a typical apparatus operation.

Initially, one or more supports are placed in one or more slots in the holder. The dispenser is then moved to a position directly above a well (not shown) containing a solution of the first reagent to be dispensed on the support(s). The dispenser solenoid is actuated now to lower the dispenser tip into this well, causing the capillary channel in the dispenser to fill. Motors 82, 100 are now actuated to position the dispenser at a selected array position at the first of the supports. Solenoid actuation of the dispenser is then effective to dispense a selected-volume droplet of that reagent at this location. As noted above, this operation is effective to dispense a selected volume preferably between 2 pl and 2 nl of the reagent solution.

The dispenser is now moved to the corresponding position at an adjacent support and a similar volume of the solution is dispensed at this position. The process is repeated until the reagent has been dispensed at this preselected corresponding position on each of the supports.

Where it is desired to dispense a single reagent at more than two array positions on a support, the dispenser may be moved to different array positions at each support, before moving the dispenser to a new support, or solution can be dispensed at individual positions

on each support, at one selected position, then the cycle repeated for each new array position.

To dispense the next reagent, the dispenser is positioned over a wash solution (not shown), and the dispenser tip is dipped in and out of this solution until the reagent solution has been substantially washed from the tip. Solution can be removed from the tip, after each dipping, by vacuum, compressed air spray, sponge, or the like.

The dispenser tip is now dipped in a second reagent well, and the filled tip is moved to a second selected array position in the first support. The process of dispensing reagent at each of the corresponding second-array positions is then carried out as above. This process is repeated until an entire microarray of reagent solutions on each of the supports has been formed.

Microarray Substrate

This section describes embodiments of a substrate having a microarray of biological polymers carried on the substrate surface, in particular a microarray of distinct polypeptides bound on a glass slide coated with a polycationic polymer is described.

A substrate is formed according to another aspect of the invention, and intended for use in detecting binding of labeled ligands to one or more of a plurality distinct biopolymers. In one embodiment, the substrate includes a glass substrate having formed on its surface, a coating of a polycationic polymer, preferably a cationic polypeptide, such as poly-lysine or poly-arginine. Formed on the polycationic coating is a microarray of distinct biopolymers, each localized at known selected array regions, such as regions.

The slide may be coated by placing a uniform-thickness film of a polycationic polymer, e.g., poly-l-lysine, on the surface of a slide and drying the film to form a dried coating. The amount of polycationic polymer added is sufficient to form at least a monolayer of polymers on the glass surface. The polymer film is bound to surface via electrostatic binding between negative silyl-OH groups on the surface and charged amine groups in the polymers. Poly-l-lysine coated glass slides may be obtained commercially, e.g., from Sigma Chemical Co. (St. Louis, Mo.).

A suitable microarray substrate is also made through chemical derivatization of glass. Silane compounds with appropriate leaving groups on a terminal Si will covalently bond to glass surfaces. A derivatization molecule can be designed to confer the desired chemistry to the surface of the glass substrate. An example of such a bifunctional reagent is amino-propyl-tri(ethoxy)silane, which reacts with glass surfaces at the tri(ethoxy)silane portion of the molecule while leaving the amino portion of the molecule free. Surfaces having terminal amino groups are suitable for adsorption of biopolymers in the same manner as poly-lysine

coated slides. The identity of the terminal surface group can be modified by further chemical reaction. For example, reaction of the terminal amine in the above example with glutaraldehyde results in a terminal aldehyde group. Further layers of modification may be applied to achieve the desired reactivity before spotting the microarray, such as by application of a Protein A or Protein G solution to the silynated glass. Additional surfaces that bind polypeptides are nitrocellulose-coated glass slides, available commercially from Schleicher and Schuell, and protein-binding plastics such as polystyrene.

The spotted polypeptides may be attached by either adsorption or covalent bonding. Adsorption occurs through electrostatic, hydrophobic, Van der Waals, or hydrogen-bonding interactions between the spotted polypeptide and the array substrate. Simple application of the polypeptide solution to the surface in an aqueous environment is sufficient to adsorb the polypeptide. Covalent attachment is achieved by reaction of functional groups on the polypeptide with a chemically activated surface. For example, if the surface has been activated with a highly reactive electrophilic group such as an aldehyde or succinimide group, unmodified polypeptides react at amine groups, as at lysine residues or the terminal amine, to form a covalent bond.

To form the microarray, defined volumes of distinct biopolymers are deposited on the polymer-coated slide, as described in Section II. According to an important feature of the substrate, the deposited biopolymers remain bound to the coated slide surface non-covalently when an aqueous sample is applied to the substrate under conditions that allow binding of labeled ligands in the sample to cognate binding partners in the substrate array.

In a preferred embodiment, each microarray contains at least 10^3 distinct polynucleotide or polypeptide biopolymers per surface area of less than about 1 cm^2. In one embodiment, the microarray contains 400 regions in an area of about 16 mm^2, or 2.5 x 10^3 regions/cm^2. Also in a preferred embodiment, the biopolymers in each microarray region are present in a defined amount between about 0.1 femtomoles and 100 nanomoles (in the case of polynucleotides). As above, the ability to form high-density arrays of this type, where each region is formed of a well-defined amount of deposited material, can be achieved in accordance with the microarray-forming method described in Section II.

Also in a preferred embodiment, the biopolymers have lengths of at least about 50 units, *e.g.* amino acids, nucleotides, *etc.*, i.e., substantially longer than polymers which can be formed in high-density arrays by various *in situ* synthesis schemes.

The polypeptide biopolymers may comprise polypeptides from any source. Polypeptides of interest include those isolated from cells or other biological sources, synthesized polypeptides, including synthesized peptides and peptides selected from combinatorial libraries, polypeptides synthesized from recombinant nucleic acids, and the

like. In one embodiment, the polypeptides are isolated from phage display libraries or clones (see Huse et al. (1989) Science. 1989 246(4935):1275-81; Winter et al. (1994) Annu Rev Immunol. 12:433-55; Clackson et al. (1991) Nature 352(6336):624-8). Usually the polypeptides on each discrete region of the array will be substantially pure.

Uses of the Microarrays

Arrays of whole cells, peptides, enzymes, antibodies, antigens, receptors, ligands, phospholipids, polymers, drug congener preparations or chemical substances can be fabricated by the means described in this invention for large scale screening assays in medical diagnostics, drug discovery, molecular biology, immunology and toxicology.

Microarrays of immobilized polypeptides prepared in accordance with the invention can be used for large scale binding assays in numerous diagnostic and screening applications. The multiplexed measurement of quantitative variation in levels of large numbers of proteins allows the recognition of patterns defined by several to many different proteins. One can simultaneously assess many physiological parameters and disease-specific patterns.

One embodiment of the invention involves the separation, identification and characterization of proteins present in a biological sample. For example, by comparison of disease and control samples, it is possible to identify "disease specific proteins". These proteins may be used as targets for drug development or as molecular markers of disease.

Polypeptide arrays are used to monitor the expression levels of proteins in a sample where such samples may include biopsy of a tissue of interest, cultured cells, microbial cell populations, biological fluids, including blood, plasma, lymph, synovial fluid, cerebrospinal fluid, cell lysates, culture supernatants, amniotic fluid, *etc.*, and derivatives thereof. Of particular interest are clinical samples of biological fluids, including blood and derivatives thereof, cerebrospinal fluid, urine, saliva, lymph, synovial fluids, *etc.* Such measurements may be quantitative, semi-quantitative, or qualitative. Where the assay is to be quantitative or semi-quantitative, it will preferably comprise a competition-type format, for example between labeled and unlabeled samples, or between samples that are differentially labeled.

Assays to detect the presence of ligands to the immobilized polypeptides may be performed as follows, although the methods need not be limited to those set forth herein.

Samples, fractions or aliquots thereof are added to a microarray comprising bound polypeptide. Samples may comprise a wide variety of biological fluids or extracts as described above. Preferably, a series of standards, containing known concentrations of control ligand(s) is assayed in parallel with the samples or aliquots thereof to serve as

controls. The incubation time should be sufficient for ligand molecules to bind the polypeptides. Generally, from about 0.1 to 3 hr is sufficient, usually 1 hr sufficing.

After incubation, the insoluble support is generally washed of non-bound components. Generally, a dilute non-ionic detergent medium at an appropriate pH, generally 7-8, is used as a wash medium. From one to six washes may be employed, with sufficient volume to thoroughly wash non-specifically bound proteins present in the sample.

In order to detect the presence of bound ligands, a variety of methods may be used. These fall into three general groups. The ligand itself may be labeled with a detectable label, and the amount of bound label directly measured. Alternatively, the labeled sample may be mixed with a differentially labeled, or unlabeled sample in a competition assay. In yet another embodiment, the sample itself is not labeled, but a second stage labeled reagent is added in order to quantitate the amount of ligand present.

Examples of labels that permit direct measurement of ligand binding include radiolabels, such as ^{3}H or ^{125}I, fluorescers, dyes, beads, chemilumninescers, colloidal particles, and the like. Suitable fluorescent dyes are known in the art, including fluorescein isothiocyanate (FITC); rhodamine and rhodamine derivatives; Texas Red; phycoerythrin; allophycocyanin; 6-carboxyfluorescein (6-FAM); 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein (JOE); 6-carboxy-X-rhodamine (ROX); 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX); 5-carboxyfluorescein (5-FAM); N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA); sulfonated rhodamine; Cy3; Cy5; *etc.* Preferably the compound to be labeled is combined with an activated dye that reacts with a group present on the ligand, e.g. amine groups, thiol groups, aldehyde groups, *etc.*

Particularly where a second stage detection is performed, for example by the addition of labeled antibodies that recognize the ligand, the label can be a covalently bound enzyme capable of providing a detectable product signal after addition of suitable substrate. Examples of suitable enzymes for use in conjugates include horseradish peroxidase, alkaline phosphatase, malate dehydrogenase and the like. Where not commercially available, such antibody-enzyme conjugates are readily produced by techniques known to those skilled in the art. The second stage binding reagent may be any compound that binds the ligands with sufficient specificity such that it can be distinguished from other components present. In a preferred embodiment, second stage binding reagents are antibodies specific for the ligand, either monoclonal or polyclonal sera, *e.g.* mouse anti-human antibodies, *etc.*

For an amplification of signal, the ligand may be labeled with an agent such as biotin, digoxigenin, *etc.*, where the second stage reagent will comprise avidin, streptavidin, anti-digoxigenin antibodies, *etc.* as appropriate for the label.

Microarrays can be scanned to detect binding of the ligands, *e.g.* by using a scanning las r microscope, by fluorimetry, a modified ELISA plate reader, *etc.* For example, a scanning laser microscope may perform a separate scan, using the appropriate excitation line, for each of the fluorophores used. The digital images generated from the scan are then combined for subsequent analysis. For any particular array element, the ratio of the fluorescent signal with one label is compared to the fluorescent signal from the other label DNA, and the relative abundance determined.

The microarrays and methods of detecting ligands may be used for a number of screening, investigative and diagnostic assays. In one application, an array of antibodies is bound to total protein from an organism to monitor protein expression for research or diagnostic purposes. Labeling total protein from a normal cell with one color fluorophore and total protein from a diseased cell with another color fluorophore and simultaneously binding the two samples to the same array allows for differential protein expression to be measured as the ratio of the two fluorophore intensities. This two-color experiment can be used to monitor expression in different tissue types, disease states, response to drugs, or response to environmental factors.

In screening assays, for example to determine whether a protein or proteins are implicated in a disease pathway or are correlated with a disease-specific phenotype, measurements may be made from cultured cells. Such cells may be experimentally manipulated by the addition of pharmacologically active agents that act on a target or pathway of interest. This application is important for elucidation of biological function or discovery of therapeutic targets.

For many diagnostic and investigative purposes it is useful to measurement levels of ligands, *e.g.* protein ligands, in blood or serum. This application is important for the discovery and diagnosis of clinically useful markers that correlate with a particular diagnosis or prognosis. For example, by monitoring a range of antibody or T cell receptor specificities in parallel, one may determine the levels and kinetics of antibodies during the course of autoimmune disease, during infection, through graft rejection, *etc.* Alternatively, novel protein markers associated with a disease of interest may be developed through comparisons of normal and diseased blood sample, or by comparing clinical samples at different stages of disease.

In another embodiment of the invention, the polypeptide arrays are used to detect post-translational modifications in proteins, which is important in studying signaling pathways and cellular regulation. Post-translational modifications can be detected using antibodies specific for a particular state of a protein, such as phosphorylated, glycosylated, farnesylated, *etc.*

The detection of these interactions between ligands and polypeptides can lead to a medical diagnosis. For example, the identity of a pathogenic microorganism can be established unambiguously by binding a sample of the unknown pathogen to an array containing many types of antibodies specific for known pathogenic antigens.

EXPERIMENTAL

It is to be understood that this invention is not limited to the particular methodology, protocols, cell lines, animal species or genera, and reagents described, as such may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

As used herein the singular forms "a", "and", and "the" include plural referents unless the context clearly dictates otherwise. All technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs unless clearly indicated otherwise.

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the subject invention, and are not intended to limit the scope of what is regarded as the invention. Efforts have been made to ensure accuracy with respect to the numbers used (*e.g.* amounts, temperature, concentrations, *etc.*) but some experimental errors and deviations should be allowed for. Unless otherwise indicated, parts are parts by weight, molecular weight is average molecular weight, temperature is in degrees centigrade; and pressure is at or near atmospheric.

EXAMPLE 1

Antibody and Antigen Microarrays

A set of antibody and antigen pairs with which highly controlled experiments could be performed was assembled, using 115 different ligand/anti-ligand pairs.

Methods

Array preparation: Antibody solutions were prepared at 100-200 µg/mL in a PBS/0.02% sodium azide buffer without glycerol. The antibodies were spotted onto glass slides treated with poly-l-lysine. The slides are derivitized by the following procedure. Place slides in slide racks, then racks in chambers. Prepare cleaning solution by dissolving 70 g NaOH in 280 mL ddH2O, then adding 420 mL 95% ethanol. Total volume is 700 mL (= 2 X 350 mL); stir until completely mixed. Pour solution into chambers with slides; cover

chambers with glass lids. Mix on orbital shaker for 2 hr. Quickly transfer racks to fresh chambers filled with ddH2O. Rinse vigorously by plunging racks up and down. Repeat rinses 4X with fresh ddH2O each time. Prepare polylysine solution: 70 mL poly-L-lysine + 70 mL tissue culture PBS in 560 mL water. Transfer slides to polylysine solution and shake 15 min. - 1 hr. Transfer rack to fresh chambers filled with ddH2O. Plunge up and down 5X to rinse. Centrifuge slides on microtiter plate carriers for 5 min. @ 500 rpm. Dry slide racks in 45° C vacuum oven for 10 min.

The antibodies and antigens were prepared in a 384-well microtitre plate containing at least three wells each of 110 different antibodies or antigens. A 16-tip print head on the arrayer spotted the plate three times for a total of 1152 spots, with 9-12 duplicate spots per antibody or antigen. The spacing between spots was 375 micrometers. The arrays were sealed in an airtight container. They can be stored at 4° C for short term storage (~1 month) or frozen for longer storage.

The back sides of the slides were marked with a diamond scribe or indelible marker to delineate the location of the spots. To remove unbound protein, the arrays were dunked several times in PBS/3% non-fat milk/0.1% Tween-20, and transferred immediately to a solution of PBS/3% non-fat milk, and let block overnight at 4° C. The milk solution was first centrifuged (10 minutes at 10000 x g) to remove particulate matter.

After blocking, the slides were dunked and thoroughly agitateed for one minute each in three consecutive room temperature washes of 0.2X PBS to remove the unbound milk protein. The arrays remained in the last wash until application of the protein mixture.

Sample preparation: Protein solutions were prepared in a 0.1 carbonate or phosphate buffer at pH 8.0, using up to ~15 μg protein per array (when using 25 μL per array) at a concentration such that after mixing with the dye solution (see below), the final protein concentration is 0.2-2 mg/mL.

NHS-ester activated Cy-dyes (Amersham, catalog # PA23001 (Cy3) and PA25001 (Cy5)) were dissolved in a 0.1 M pH 8.0 carbonate buffer so that the final concentration of the dye after mixing with the protein solution was 100-300 μM. (Each vial of dye contains 200 nmols.) The dye and protein solutions were mixed, and allowed to react in the dark at room temperature for 45 minutes. The reference protein solution was mixed with the Cy3 dye solution, and the test protein solution with the Cy5 dye solution. The reactions were quenched by adding enough 1 M pH 8 tris or glycine to each so that at least a 200-fold excess of quencher:dye concentration was achieved.

Each mix was loaded into a microconcentrator having the appropriate molecular weight cutoff. A 3000 D cutoff captures most proteins while still removing the dye. If smaller

proteins are not important, the 10000 D cutoff is faster. The mix was centrifuged according to the microconcentrator instructions. The 10000 D microcon typically requires 20 minut s and the 3000 D microcon requires 80 minutes of centrifugation at 10000 x g and room temperature. After centrifuging, 3% milk blocker was added to either the Cy5 or Cy3-labeled protein mixes. (The milk must first be centrifuged to remove particulate matter: 10 minutes at 10000 x g.) Add 25 μL milk for each array to be generated from the protein mix. PBS was added to each microcon to a 500 μL volume, and centrifuged again. The concentrated samples were collected into a small volume (~5 μL) of PBS to prevent drying and precipitation.

The Cy3-labeled reference protein solution was distributed to the appropriate Cy5-labeled test protein solutions, and PBS added to each mix to achieve a volume of 25 μL per array. Particulate matter or precipitate was removed by 1) filtering with a 0.45 μm spin filter, or 2) centrifuging 10 minutes at 14000 x g and pipetting out the supernatant.

Detection: Each array was removed individually from the PBS wash. Without allowing the array to dry, 25 μL of the dye-labeled protein solution was placed over the spots (within the marked boundaries), with a cover slip placed over the protein solution. The cover slip has dimensions at least ¼ inch longer than the dimensions of the array. The arrays were placed in a sealed humidification chamber with a layer of PBS under the arrays, and incubated at 4° C for approximately two hours. Each array was briefly dunked in PBS to remove the protein solution and the cover slip, and transfered immediately to a slide rack in a PBS/0.1% Tween-20 solution. After all the arrays have been racked in the PBS/Tween solution, they were washed on an orbital shaker for ~20 minutes at room temperature. The arrays were transferred to a new rack (to minimize Tween carryover) in a PBS solution and rocked gently for 5-10 minutes, then transferred to wash solutions of PBS, H_2O, and H_2O for five minutes each of gentle agitation. The arrays were then spin-dried and scanned.

Analysis: The fluorescence intensity at each spot reflects the level of binding to that particular protein. The relative concentration between proteins in differentially dye-labeled pools is determined by comparing the fluorescence intensities between the color channels at each spot. The following method is used to determine relative concentrations.

The location of each analyte spot on the array is outlined using "gridding" software, such as GenePix or ScanAlyze, which places a boundary around each spot on the array.

The fluorescence signal from each spot is determined as the average or median of the pixel intensities within the boundary outlined using the gridding software. Each color channel is treated independently. Optionally statistical methods are used to reject "outli r"

pixels within the circle, i.e. pixels that have intensities significantly outside the average pixel intensity.

The background is subtracted from the signal. The background may be determined as 1) the median or average of pixel intensities from the local area around each spot, or as 2) the median or average or pixel intensities from within certain spots or areas determined to be non-binding background areas. Statistical methods may be used to reject outlier pixels in the background.

The relative binding at each spot between proteins in the separately labeled pools is equivalent to the ratio of fluorescence intensities in the two color channels. In order for the ratio to reflect the true relative concentrations, the background-subtracted signal from one of the color channels must be multiplied by a normalization factor. The normalization factor may be determined by selecting spots for which the true concentrations are known and calculating the factor that most accurately returns the true color ratio. Alternatively, if no control spots are used, one may assume that the average binding across every spot on the array is roughly equal for the two protein pools. A normalization factor is then calculated that gives an average color ratio of one for all the spots on the array.

Once all arrays have been normalized and color ratios have calculated, changes in protein concentration from array to array may be compared. Interpretation is simplest if the same reference pool is used for each experiment.

Results:

To test the specificity, quantitation, and limits of detection of the protein array, six mixes of antigens were made in which the concentration of each protein varied uniquely across the mixes. For example, one protein changed from high to low concentration, another from low to high, and another from low to high to low. The concentrations varied three orders of magnitude over the whole set. This set of six mixes was detected at various concentrations and in various levels of fetal calf serum (FCS) background. The ability to reconstruct the actual concentration changes from the data indicated the level of performance of the microarrays.

Microarrays were constructed containing 6 to 9 duplicate spots from each antibody. Figure 5 presents a series of these arrays generated from the set of six unique protein mixes (labeled with the red-fluorescing dye Cy5) compared against a reference mix (labeled with the green-fluorescing dye Cy3) containing an equal amount of each protein. For each spot on the array, the red/green ratio was calculated and then plotted as a function of dilution. Figure 6 presents plots of the log of the red-to-green ratio (R/G) versus dilution for eight of the antigens. The ideal slope, calculated as the log of the concentration ratio of the proteins,

is shown as a straight solid line decreasing from 1.5 to –1.5. The other lines on the graph represent duplicate spots on the array. The slopes of the experimental data are very similar to the ideal slope over the six concentrations tested, indicating that these antibodies detected the cognate antigens specifically and quantitatively. Deviations from ideal slope appear to occur systematically between the duplicate spots, suggesting that the largest error in quantitation occurred in pipetting or data reduction rather than in random variability in the system.

The detection of a specific protein is limited not only by concentration, but also by the concentration of background proteins. To determine how well specific proteins can be detected in high protein background, the set of unique protein mixes was spiked into varying amounts of FCS before dye labeling. FCS concentrations 10 times greater and 100 times greater than the antigen mix concentration were used. Figure 7 shows the effect of protein background on quantitation for the proteins IgG and flag. Without the serum background, accurate quantitation is observed for both proteins over the entire concentration range, which was from 120 ng/mL to 120 pg/mL. At the 10x serum concentration, the flag protein still shows accurate quantitation, but IgG shows slight deviation from the ideal slope at the high and low limits. At the 100x serum concentration, both proteins exhibit marked deviations from the ideal slope. The partial concentrations (the antigen concentration divided by the total protein concentration) ranged from 4×10^{-5} to 4×10^{-8} for the 100x serum trial. Thus the partial concentration detection limit is $\sim 2 \times 10^{-8}$ for flag and $\sim 2 \times 10^{-7}$ for IgG using these antibodies. These partial concentrations are in a physiological range for many clinically interesting blood serum proteins. The results of this type of analysis for each antigen tested are presented in the table below. Antibodies were classified according to the presence of accurate quantitation over the entire range for all of the low background trial and at least part of the higher background trials (++). They were classified as (+) if they showed accurate quantitation for most of the low background trial. Many of the antibodies showed either no signal or non-specific signal.

In a second mode of detection, antigens were spotted onto the array to detect labeled antibodies. Figure 7 presents an example of specific detection of antibodies in four unique mixes. A combinatorial labeling scheme was employed that enabled identification of specific antigen/antibody binding. An analysis similar to that described above was carried out to classify the binding specificity of antigens on the microarray. The results of that analysis are presented in the table below along with the antibody array results. According to this analysis, the protein array works at least as well or better using spotted antigens as compared to spotted antibodies.

Antibody/antigen	Antibody array ++	+	-	Part. conc. limit	Antigen array ++	+	-
Anti-AIM-1	x			1.00E-06	x		
Anti-HCG	x				x		
Anti-MAP4	x				x		
Anti-Per2	x				x		
Anti-Flag (new)	x						x
Anti-Alpha HCG	x			4.00E-08		x	
Anti-Fc. IgG	x			1.00E-07			x
Anti-Flag (old)	x						
Anti-Human IgG	x						
Anti-Mint2	x					x	
Anti-Sin	x						x
Anti-SOD	x					x	
Anti-ABR		x		6.00E-05	x		
Anti-AKAP-KL		x			x		
Anti-Dematin		x		1.00E-04	x		
Anti-Dlg		x			x		
Anti-DSIF		x			x		
Anti-FIN13		x			x		
Anti-HDAC3		x			x		
Anti-HIF-1alpha		x			x		
Anti-ICH-IL		x			x		
Anti-IGF2R		x			x		
Anti-Kanadaptin		x			x		
Anti-La		x			x		
Anti-LAIR-1		x			x		
Anti-LAP2		x			x		
Anti-MEKK3		x			x		
Anti-Mint1		x			x		
Anti-MST3		x			x		
Anti-p19 Skp1		x			x		
Anti-p38 gamma		x			x		
Anti-Rab4		x			x		
Anti-TEF-1		x			x		
Anti-ZO-1		x			x		

Anti-Tropomyosin		x					
Anti-Alkaline phosphatase		x				x	
Anti-cTnI		x		4.00E-04		x	
Anti-DFF45		x				x	
Anti-Fibronectin		x				x	
Anti-GOK		x					x
Anti-GS15		x				x	
Anti-Insulin		x				x	
Anti-LAT		x				x	
Anti-MAD-3		x					
Anti-mGluR1		x				x	
Anti-MST1		x				x	
Anti-Myoglobin (ResGen)		x				x	
Anti-Myoglobin (Sigma)		x					
Anti-Neuroglycan C		x				x	
Anti-PSA 2F5		x				x	
Anti-PSA F5		x					
Anti-Rad50		x				x	
Anti-RBC		x					x
Anti-Rim		x				x	
Anti-ROCK-1		x					x
Anti-SRPK1		x					x
Anti-VLA-3alpha		x					x
Anti-Adaptin alpha			x		x		
Anti-Bax			x		x		
Anti-Calretinin			x		x		
Anti-c-Cbl			x		x		
Anti-Clathrin H			x		x		
Anti-DEK			x		x		
Anti-DGK0			x		x		
Anti-Efp			x		x		
Anti-erg2			x		x		
Anti-hHR23B			x		x		
Anti-Kalinin B1			x		x		
Anti-PUNTS			x		x		

Anti-RNCAM		x	x			
Anti-SRP54		x	x			
Anti-TFII-I		x	x			
Anti-TIF2		x	x			
Anti-TSP-1		x	x			
Anti-VHR		x	x			
Anti-AKAP149		x		x		
Anti-alpha acid (AGP)	glycoprotein	x			x	
Anti-Annexin II		x			x	
Anti-ARNT1		x		x		
Anti-Brm		x			x	
Anti-Calmodulin		x			x	
Anti-Calnexin		x			x	
Anti-CaM K IV		x		x		
Anti-CAS		x				
Anti-CLA-1		x			x	
Anti-CRP		x			x	
Anti-Cyclin A		x				
Anti-DNA pol delta		x		x		
Anti-eIF-5		x		x		
Anti-ERp72		x		x		
Anti-ESA		x			x	
Anti-G3VP		x		x		
Anti-Gelsolin		x		x		
Anti-Hsp70		x			x	
Anti-Hsp90		x			x	
Anti-IAK-1		x		x		
Anti-IQGAP1		x			x	
Anti-KAP3A		x			x	
Anti-Ki-67		x			x	
Anti-LRP		x			x	
Anti-MEK5		x			x	
Anti-Neurabin		x		x		
Anti-Numb		x		x		
Anti-PARP		x		x		

Anti-Pax-5			x				x
Anti-PDI			x				x
Anti-PI3-K p170			x			x	
Anti-rSec8			x			x	
Anti-SIRPalpha1			x				x
Anti-Smad4			x				x
Anti-TAF-172			x				x
Anti-TIAR			x			x	
Anti-Transportin			x				x
Anti-Utrophin			x				x

it is apparent from the above experimental data and descriptions that the subject methods provide a useful method for constructing a microarray comprising immobilized polypeptides. The polypeptides retain the binding specificity, and are useful in the detection and quantitation of ligands that bind to polypeptides, including proteins and fragments thereof, peptides, nucleic acids, factors and co-factors, and the like.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

WHAT IS CLAIMED IS:

1. A method of simultaneously detecting the presence of multiple protein-binding ligands in a sample, the method comprising:

contacting said sample with a microarray of polypeptides, wherein said microarray comprises 100 or more discrete regions of distinct polypeptide strands per cm^2 of solid planar support;

washing said support free of unbound sample; and

detecting the presence of bound ligands.

2. The method of Claim 1, wherein the ligands present in said sample are labeled with a detectable label.

3. The method of Claim 2, wherein said detectable label is a fluorochrome.

4. The method of Claim 2, further comprising contacting said microarray with a second sample comprising ligands labeled with a second detectable label.

5. The method of Claim 4, wherein said second detectable label is a fluorochrome.

6. The method according to Claim 1, wherein said sample is a clinical sample of a physiological fluid.

7. The method according to Claim 6, wherein said physiological fluid is blood or a derivative thereof.

8. The method of Claim 1, wherein said sample is a cell culture supernatant.

9. The method of Claim 1, wherein said sample is a cell lysate.

10. The method according to Claim 1, wherein said polypeptides are antibodies.

11. The method of Claim 1, wherein said polypeptides are antigens.

12. The method of Claim 1, wherein said polypeptides are at least 50 amino acids in length.

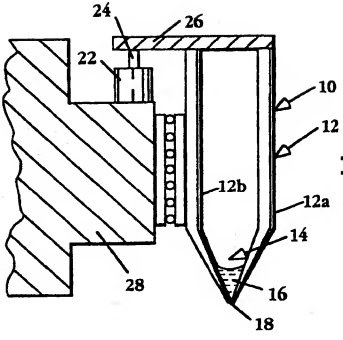


Fig. 1

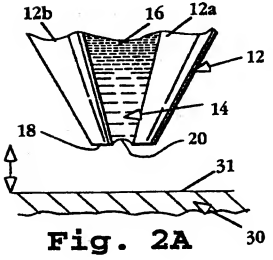


Fig. 2A

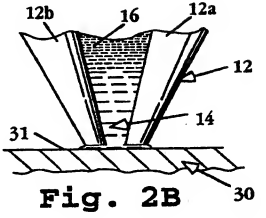


Fig. 2B

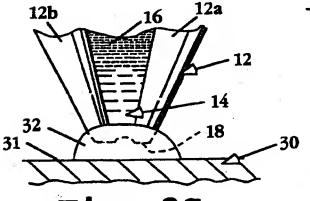


Fig 2C

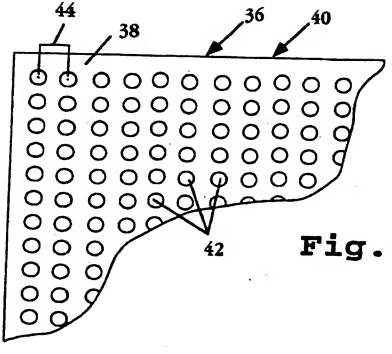


Fig. 3

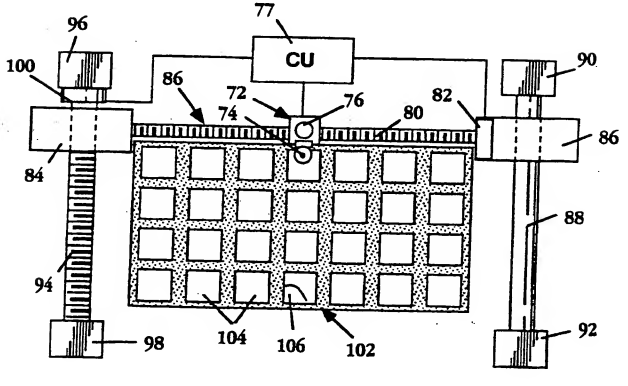


Fig. 4

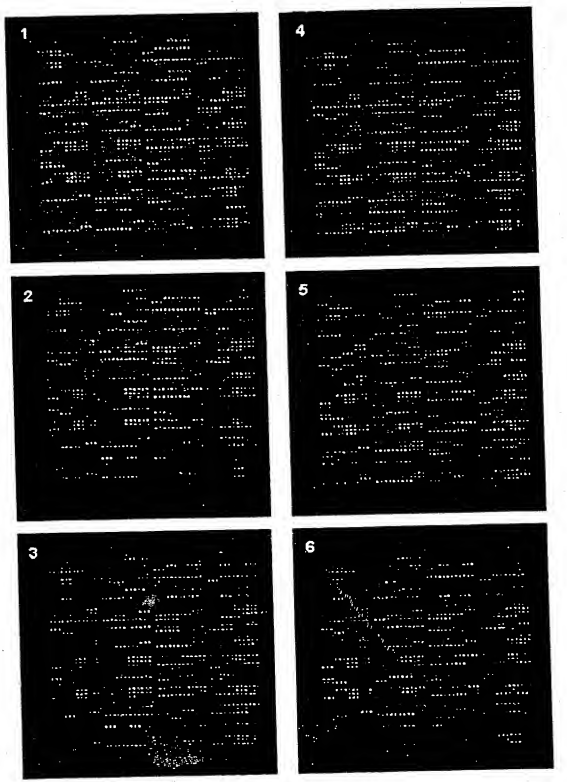


FIGURE 5

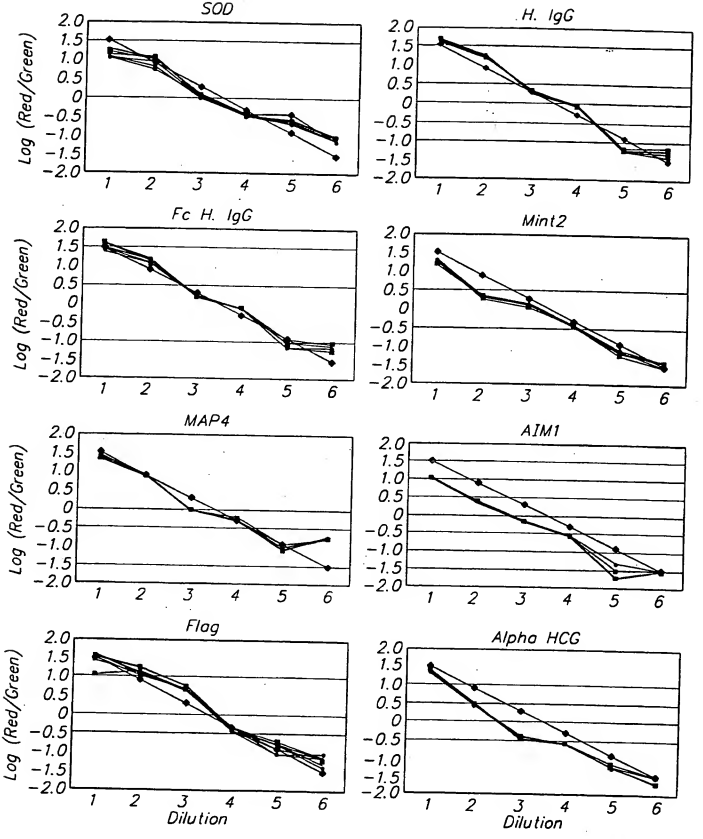


FIGURE 6

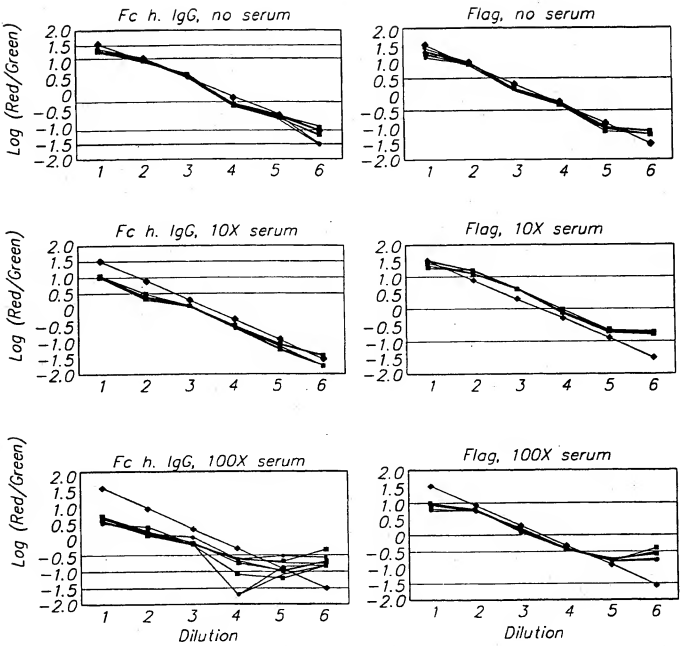


FIGURE 7

	mix 1	mix 2	mix 3	mix 4
AKAP-KL	1	2	3	2
LAIR-1	1	2	2	3
ABR	3	1	2	3

0 = blank
1 = green
2 = red
3 = yellow

FIGURE 8

INTERNATIONAL SEARCH REPORT

In tional Application No
PCT/US 00/10171

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 G01N33/68 B01J19/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 G01N B01J

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 5 807 522 A (PATRICK O. BROWN & TIDHAR DARI SHALON) 15 September 1998 (1998-09-15) column 3, line 23 - line 35 column 4, line 17 - line 23 column 6, line 32 - line 37 column 14, line 19 - line 34 column 15, line 5 - line 58	1-12
X	WO 97 42507 A (ISIS INNOVATION LIMITED) 13 November 1997 (1997-11-13) abstract page 3, line 15 -page 4, line 16 page 7, line 18 - line 25 page 9, line 14 -page 10, line 3 page 4, line 14 - line 26	1-12

-/—

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

A document defining the general state of the art which is not considered to be of particular relevance

E earlier document but published on or after the international filing date

L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

O document referring to an oral disclosure, use, exhibition or other means

P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

& document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
11 October 2000	18/10/2000

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Stevnsborg, N

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 5 324 633 A (STEPHEN P.A. FODOR & LAURA T. MAZZOLA) 28 June 1994 (1994-06-28) abstract column 3, line 47 - line 60 column 5, line 21 - line 38 column 6, line 3 - line 61 column 10, line 21 -column 11, line 17	1-12
X	JEFFREY W. JACOBS & STEPHEN P.A. FODOR: "COMBINATORIAL CHEMISTRY - APPLICATIONS OF LIGHT DIRECTED CHEMICAL SYNTHESIS" TIBTECH, vol. 12, no. 1, 1994, pages 19-26, XP000652268 CAMBRIDGE, UK the whole document	1-12
X	STEPHEN P.A. FODOR ET AL.: "LIGHT-DIRECTED, SPATIALLY ADDRESSABLE PARALLEL CHEMICAL SYNTHESIS" SCIENCE, vol. 251, no. 4995, 15 February 1991 (1991-02-15), pages 767-773, XP000486899 US ISSN: 0036-8075 cited in the application the whole document	1-12
X	S. M. RUBER ET AL.: "LIGHT-DIRECTED COMBINATORIAL PEPTIDE SYNTHESIS" 1992 , PROCEEDINGS OF THE 12TH AMERICAN PEPTIDE SYMPOSIUM, 16-21 JUNE 1991, CAMBRIDGE, MA, USA , LEIDEN, NL XP000371924 185690 page 489 -page 491	1-12
X	RONALD FRANK : "SPOT-SYNTHESIS: AN EASY TECHNIQUE FOR THE POSITIONALLY ADDRESSABLE, PARALLEL CHEMICAL SYNTHESIS ON A MEMBRANE SUPPORT" TETRAHEDRON, vol. 48, no. 42, 16 October 1992 (1992-10-16), pages 9217-9232, XP000353580 UK ISSN: 0040-4020 page 9217 -page 9232	1-12

-/—

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	CHRISTOPHER P. HOLMES ET AL.: "THE USE OF LIGHT-DIRECTED COMBINATORIAL PEPTIDE SYNTHESIS IN EPITOPE MAPPING" BIOPOLYMERS (PEPTIDE SCIENCE), vol. 37, no. 3, 1995, pages 199-211, XP000654595 NEW YORK, US ISSN: 0006-3525 page 199 -page 211	1-12

1

INTERNATIONAL SEARCH REPORT

Information on patent family members

Int ional Application No
PCT/US 00/10171

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
US 5807522 A	15-09-1998	AT 180570 T	15-06-1999
		AU 709276 B	26-08-1999
		AU 2862995 A	15-01-1996
		CA 2192095 A	28-12-1995
		DE 69509925 D	01-07-1999
		DE 69509925 T	09-12-1999
		EP 0804731 A	05-11-1997
		EP 0913485 A	06-05-1999
		ES 2134481 T	01-10-1999
		GR 3030430 T	30-09-1999
		JP 10503841 T	07-04-1998
		US 6110426 A	29-08-2000
		WO 9535505 A	28-12-1995
WO 9742507 A	13-11-1997	NONE	
US 5324633 A	28-06-1994	NONE	